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		Match	%				
1	432	100.0	432	2	QV785690	Sequence	QV785690 Sequence
2	432	100.0	432	2	AY692896	Saccharom	AY692896 Saccharom
3	432	100.0	718	4	S45268	TTT-thioltr	S45268 TTT-thioltr
4	432	100.0	932	2	AX536532	Sequence	AX536532 Sequence
5	432	100.0	72119	4	SCD97717	U33057	U33057 Saccharomyc
6	151.6	35.1	110000	4	CR380957.05	Continuation (6 of	Continuation (6 of
7	147.4	34.1	833	2	AX536464	Sequence	AX536464 Sequence
8	147.4	34.1	316613	4	CSCHRII	U33057	U33057 Saccharomyc
9	147	34.0	994	7	CNS06347	AL401117 T7 end of	AL401117 T7 end of
10	143.4	31.2	3333	2	QV785688	Sequence	QV785688 Sequence
11	137.6	31.9	110000	4	CR382123.00	Continuation (2 of	Continuation (2 of
12	137.6	31.9	110000	4	CR382123.01	Continuation (2 of	Continuation (2 of
13	89	20.6	360	2	AX489480	Sequence	AX489480 Sequence
14	89	20.6	360	2	AX537006	Sequence	AX537006 Sequence
15	83.8	19.4	110000	4	CR382129.06	Continuation (7 of	Continuation (7 of
16	80.2	18.6	110000	4	AE016819.17	Continuation (18 of	Continuation (18 of
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18	69.8	16.2	582	2	AR548881	Sequence	AR548881 Sequence


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ORIGIN
Query Match 100.0%; Score 432; DB 4; Length 718;
Best Local Similarity 100.0%; Pred. No. 5e-123;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGACCAATTTTCTTCGACTCGAATTTAATGTTATTTATCATTTACAGCTTGT 60
DB 108 ATGGAGACCAATTTTCTTCGACTCGAATTTAATGTTATTTATCATTTACAGCTTGT 167
QY 61 GCCACAAGAAATTTATGCTAAAGATTTTATCTACTCCAAAAATGGTATCCAGGAACA 120
DB 168 GCCACAAGAAATTTATGCTAAAGATTTTATCTACTCCAAAAATGGTATCCAGGAACA 227
QY 121 GTTGCTCAGTAAAGATCTGATGGCCAAAAGAGTGTGTTGTCAGCAAGACATAC 180
DB 228 GTTGCTCAGTAAAGATCTGATGGCCAAAAGAGTGTGTTGTCAGCAAGACATAC 287
QY 181 TGCCTTACTGTAAGCTACTTTGCTACCTCTTCCAAAGATTTGAACGTTCCCAATCC 240
DB 288 TGCCTTACTGTAAGCTACTTTGCTACCTCTTCCAAAGATTTGAACGTTCCCAATCC 347
QY 241 AAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGAGCGTTTA 300
DB 348 AAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGAGCGTTTA 407
QY 301 GAAGAAATCTCGGCCCAAAAACTGTACCTAAAGTATGATGATGAGCAATGGCTCAGAGATTCAAGAGCGTTTA 360
DB 408 GAAGAAATCTCGGCCCAAAAACTGTACCTAAAGTATGATGATGAGCAATGGCTCAGAGATTCAAGAGCGTTTA 467
QY 361 GGTAAACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420
DB 468 GGTAAACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 527
QY 421 GTATTTCATAG 432
DB 528 GTATTTCATAG 539

RESULT 4
AX536532
LOCUS AX536532 932 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 133 from Patent WO02064766.
ACCESSION AX536532
VERSION AX536532.1 GI:25262936
KEYWORDS
SOURCE
ORGANISM Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

REFERENCE
1
AUTHORS Contreras,R.H., Eberhardt,I., Luyten,W.H. and Reekmans,R.J.
TITLE Bax-responsive genes for drug target identification in yeast and
JOURNAL fungi
PATENT Patent: WO 02064766-A 133 22-AUG-2002;
FEATURES
LOCATION/Qualifiers
SOURCE 1. .932

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ORIGIN
Query Match 100.0%; Score 432; DB 2; Length 932;
Best Local Similarity 100.0%; Pred. No. 4.9e-123;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGACCAATTTTCTTCGACTCGAATTTAATGTTATTTATCATTTACAGCTTGT 60
DB 501 ATGGAGACCAATTTTCTTCGACTCGAATTTAATGTTATTTATCATTTACAGCTTGT 560
QY 61 GCCACAAGAAATTTATGCTAAAGATTTTATCTACTCCAAAAATGGTATCCAGGAACA 120
DB 561 GCCACAAGAAATTTATGCTAAAGATTTTATCTACTCCAAAAATGGTATCCAGGAACA 620
QY 121 GTTGCTCAGTAAAGATCTGATGGCCAAAAGAGTGTGTTGTCAGCAAGACATAC 180
DB 621 GTTGCTCAGTAAAGATCTGATGGCCAAAAGAGTGTGTTGTCAGCAAGACATAC 680
QY 181 TGCCTTACTGTAAGCTACTTTGCTACCTCTTCCAAAGATTTGAACGTTCCCAATCC 240
DB 681 TGCCTTACTGTAAGCTACTTTGCTACCTCTTCCAAAGATTTGAACGTTCCCAATCC 740
QY 241 AAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGAGCGTTTA 300
DB 741 AAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGAGCGTTTA 800
QY 301 GAAGAAATCTCGGCCCAAAAACTGTACCTAAAGTATGATGATGAGCAATGGCTCAGAGATTCAAGAGCGTTTA 360
DB 801 GAAGAAATCTCGGCCCAAAAACTGTACCTAAAGTATGATGATGAGCAATGGCTCAGAGATTCAAGAGCGTTTA 860
QY 361 GGTAAACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420
DB 861 GGTAAACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 920
QY 421 GTATTTCATAG 432
DB 921 GTATTTCATAG 932

RESULT 5
SCD9717
LOCUS SCD9717 72119 bp DNA linear PLN 22-OCT-2002
DEFINITION Saccharomyces cerevisiae chromosome IV cosmids 8166, 9787, 9717,
and lambda 3073.
ACCESSION U33057.271256
VERSION U33057.1 GI:927764
KEYWORDS
SOURCE
ORGANISM Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

REFERENCE
1 (bases 1 to 72119)
AUTHORS Dietrich,F.S., Mulligan,J., Allen,E., Araujo,R., Aviles,E.,
Berno,A., Carpenter,J., Chen,E., Cherry,J.M., Chung,E., Duncan,M.,
Hunicke-Smith,S., Hyman,R., Komp,C., Lashkari,D., Law,H., Lin,D.,
Mosedale,D., Nakahara,K., Namath,A., Oefner,E., Oh,C., Petel,F.X.,
Roberts,D., Schramm,S., Schroeder,M., Shogren,T., Shroff,N.,
Winant,A., Yelton,M., Botstein,D. and Davis,R.W.
TITLE The sequence of Saccharomyces cerevisiae chromosome IV right
JOURNAL Unpublished (1995)
REFERENCE 2 (bases 1 to 72119)
AUTHORS Dietrich,F.S.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1995) Department of Genetics, Stanford
University, Stanford, CA 94305-5120, USA
REFERENCE 3 (bases 1 to 72119)
AUTHORS Jia,X. and Cherry,J.M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1997) Department of Genetics, Stanford
University, Saccharomyces Genome Database, Stanford, CA 94305-5120,
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Query Match      100.0%; Score 432; DB 4; Length 72119;
Best Local Similarity 100.0%; Pred. No. 2.7e-123; Indels 0; Gaps 0;
Matches 432; Conservative 0; Mismatches 0;

Qy 1 ATGAGAGCAATTTTTCCTTCGACTCGAATTTTAAATTTTATTTATTCATTATCAGTTGTTT 60
Db 33289 ATGAGAGCAATTTTTCCTTCGACTCGAATTTTAAATTTTATTTATTCATTATCAGTTGTTT 33348

Qy 61 GCCACAAGAAATTATGCTAAAGATTTTATCTACTCCAAAATGGTATCCAGGAACA 120
Db 33349 GCCACAAGAAATTATGCTAAAGATTTTATCTACTCCAAAATGGTATCCAGGAACA 33408

Qy 121 GTGCTCACGTAAAGATCTGATTGGCCAAAAGGAAGTGTGTTCGAGCAAGACATAC 180
Db 33409 GTTGCTCACGTAAAGATCTGATTGGCCAAAAGGAAGTGTGTTCGAGCAAGACATAC 33468

Qy 181 TGCCCTTACTGTAAGCTACTTGTCTACCCCTCTTCCAGAATTTGAACGTTCCCAATCC 240
Db 33469 TGCCCTTACTGTAAGCTACTTGTCTACCCCTCTTCCAGAATTTGAACGTTCCCAATCC 33528

Qy 241 AAGCCCTTGTGTGGAAATTAGATGAATGAGCAATGGCTCAGAGATCAAGACGCTTTA 300
Db 33529 AAGCCCTTGTGTGGAAATTAGATGAATGAGCAATGGCTCAGAGATCAAGACGCTTTA 33588

Qy 301 GAAGAAATCTCGGCCAAAACCTGTACCTAACGTATACATCAATGCGCAAGCATTTGGT 360
Db 33589 GAAGAAATCTCGGCCAAAACCTGTACCTAACGTATACATCAATGCGCAAGCATTTGGT 33648

Qy 361 GGTAAACAGCATTTGGAACCTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420
Db 33649 GGTAAACAGCATTTGGAACCTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 33708

Qy 421 GTATTTCAATAG 432
Db 33709 GTATTTCAATAG 33720

RESULT 6
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WPCOMMENT
Sequence split into 13 fragments LOCUS CR380957 Accession CR380957
Fragment Name      Begin      End
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CR380957_03        300001
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CR380957_05        500001
CR380957_06        600001
CR380957_07        700001
CR380957_08        800001
CR380957_09        900001
CR380957_10       1000001
CR380957_11       1100001
CR380957_12       1200001
CR380957_13       1300001
Continuation (6 of 13) of CR380957 from base 500001 (CR380957 Candida glabrata strain CBS
Query Match      35.1%; Score 151.6; DB 4; Length 110000;
Best Local Similarity 66.8%; Pred. No. 4.8e-36; Indels 0; Gaps 0;
Matches 217; Conservative 0; Mismatches 109;

Qy 100 AAAATGGTATCCCGAGAAACAGTTGCTCAGCTAAGAGATCTGATTGGCCAAAAGGAAGTG 159
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Qy 160 TTGTTGCGAGCAAGACATACCTGCTTACTGTGTAAGCTACTTTGTCTACCTCTTCCAA 219
Db 69381 TTGTTGCTTCAAAGCTTACTGCTCCCTTACTGCGAGCTGCTAAGCAAAACCTGTTGCAA 69440

Qy 220 GAATTCAGCGTTCCCAATCCAGGCGCTTGTGTTGGAATTAGATGAATGAGCAATGGC 279
Db 69441 GAATTCAGGCTCCCAATCCAGGCGCTGCTGTTCTAGAAATTGGCAAAATTTGAAGAAAGGT 69500

Qy 280 TCAGAGATTCAGACGCTTTAGAGAAATCTCGGGCCAAAACCTGTACCTAAGCTATAC 339
Db 69501 AGCGACATTCACACGCTTTGGCTGAAATCAACGCTCAAAACACTGTCCCAATATTATC 69560

Qy 340 ATCAATGGCAAGCACATTTGTTGTTAAACAGCATTTTGGAAATTTGAAGAAAAATGGCAAG 399
Db 69561 ATCGATGGTCAACACATTTGTTGTTAAACAGTGACCTACAAAAATTTAAAGCAACCGGTAAA 69620

Qy 400 TTAGCTGAAATATTGAAGCGGTATT 425
Db 69621 CTACAACCATTTGTACAAAAGGTTTT 69646

RESULT 7
AX536464
LOCUS
DEFINITION      Sequence 65 from Patent WO02064766.
ACCESSION      AX536464
VERSION        AX536464.1 GI:25262863
KEYWORDS
SOURCE          Saccharomyces cerevisiae (baker's yeast)
ORGANISM        Saccharomyces cerevisiae
                Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
REFERENCE
1
AUTHORS         Contreras,R.H., Eberhardt,I., Luyten,W.H. and Reekmans,R.J.
TITLE           Bax-responsive genes for drug target identification in yeast and
                fungi
JOURNAL         Patent: WO 02064766-A 65 22-AUG-2002;
                JANSSEN PHARMACEUTICA N.V. (BE)
FEATURES
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Query Match      34.1%; Score 147.4; DB 2; Length 833;
Best Local Similarity 65.2%; Pred. No. 1.9e-34; Indels 0; Gaps 0;
Matches 217; Conservative 0; Mismatches 116;

Qy 99 AAAATGGTATCCCGAGAAACAGTTGCTCAGCTAAGAGATCTGATTGGCCAAAAGGAAGT 158
Db 497 AAAATGGTATCTCAAGAAACTATCAAGCAAGCTCAAGACCTTTATTCAGAAAACGAGAT 556

Qy 159 GTTTGTTGCAAGCAAGACATCTGCCCTTACTGCTAAAGCTACTTTGTCTACCTCTTCCA 218
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Db	557	CTTCGTGCATCCAAACGACTGTCCATACCTGCCATGCAGCCCTAAACACGCGTTTTTGA	616	JOURNAL PUBMED AUTHORS	seven open reading frames including the RVS161, ADP1 and PGK genes
Qy	219	AGAATTGAACGTTCCAAATCCAAAGCCCTTGTTGGATTAGATGAATGACGAATGG	278	REFERENCE	Yeast 8 (5), 409-417 (1992)
Db	617	AAAGTTAAAGGTTCCCAAGTCTCGTTGTTTGGCAATTGAATGACATGAAGAAGG	676	REFERENCE	8
Qy	279	CTCAGAGATTCAAGCGCTTTAGAAGAAATCTCGGCCCAAAACCTGTACCTAACGTATA	338	TITLE	Oliver, S.G., van der Aart, Q.J., Agostoni-Carbone, M.L., Aigle, M.,
Db	677	CGCAGACATTCAGGCTCGCTATATAGATTAAATGGCCAAAGAACCGTGCACAACTCTA	736	JOURNAL PUBMED AUTHORS	Alberghina, L., Alexandraki, D., Antoine, G., Anwar, R., Ballesta, J.P.,
Qy	339	CATCAATGGCAAGCACATTCGTGGTAAACAGCGATTTCGGAACTTTGAAGAAAATGGCAA	398	REFERENCE	Benit, P. et al.
Db	737	TATTATGTTAAACATATTGGAGCGACGACGACTTCGAGCAATTGAGGAGACTGGTGA	796	TITLE	The complete DNA sequence of yeast chromosome III
Qy	399	GTTAGCTGAATATTGAAGCCGCTATTTCATA	431	JOURNAL PUBMED AUTHORS	Nature 357 (6373), 38-46 (1992)
Db	797	ATTGAGGAATTCTAGAACCTATTCTTGCAA	829	REFERENCE	1574125
RESULT 8					
SCCHRII/c					
LOCUS	SCCHRIII	316613 bp	DNA linear	PLN 18-APR-2005	
DEFINITION	S.cerevisiae chromosome III complete DNA sequence.				
ACCESSION	X59720	S43845	S49180	S58084	S93798
VERSION	X59720.2	GI:14588895			
KEYWORDS	chromosome.				
SOURCE	Saccharomyces cerevisiae (baker's yeast)				
ORGANISM	Saccharomyces cerevisiae				
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
AUTHORS	Saccharomycetales; Saccharomycetaceae; Saccharomyces.				
TITLE	Rad, M.R., Lutzenkirchen, K., Xu, G., Kleinhans, U. and Hollenberg, C.P.				
JOURNAL	The complete sequence of a 11,953 bp fragment from CIG on				
PUBMED	chromosome III encompasses four new open reading frames				
AUTHORS	Yeast 7 (5), 533-538 (1991)				
REFERENCE	1897318				
AUTHORS	Biteau, N., Frenaux, C., Hebrard, S., Menara, A., Aigle, M. and				
TITLE	Crouzet, M.				
JOURNAL	The complete sequence of a 10.8kb fragment to the right of the				
PUBMED	chromosome III centromere of Saccharomyces cerevisiae				
AUTHORS	Yeast 8 (1), 61-70 (1992)				
REFERENCE	1580102				
TITLE	Wilson, C., Bergantino, E., Lanfranchi, G., Valle, G., Carignani, G. and				
JOURNAL	Frontali, L.				
PUBMED	A putative serine/threonine protein kinase gene on chromosome III				
AUTHORS	of Saccharomyces cerevisiae				
REFERENCE	Yeast 8 (1), 71-77 (1992)				
TITLE	Benit, P., Chanet, R., Fabre, F., Faye, G., Fukuhara, H. and Sor, F.				
JOURNAL	Sequence of the sup61-RAD18 region on chromosome III of				
PUBMED	Saccharomyces cerevisiae				
AUTHORS	Yeast 8 (2), 147-153 (1992)				
TITLE	1561837				
JOURNAL	Bolle, P.A., Gilliquet, V., Berben, G., Dumont, J. and Hilger, F.				
PUBMED	Sequence of the K3B, a 7.9 kb fragment between PGK1 and				
AUTHORS	CRX1 on chromosome III, reveals the presence of seven open reading				
TITLE	frames				
JOURNAL	Yeast 8 (3), 205-213 (1992)				
PUBMED	1574926				
AUTHORS	Sor, F., Cheret, G., Fabre, F., Faye, G. and Fukuhara, H.				
TITLE	Sequence of the HWR region on chromosome III of Saccharomyces				
JOURNAL	cerevisiae				
PUBMED	Yeast 8 (3), 215-222 (1992)				
AUTHORS	1574927				
TITLE	Skala, J., Purnelle, B. and Goffeau, A.				
JOURNAL	The complete sequence of a 10.8 kb segment distal of SUP2 on the				
PUBMED	right arm of chromosome III from Saccharomyces cerevisiae reveals				
AUTHORS					
TITLE					

JOURNAL PUBMED AUTHORS	seven open reading frames including the RVS161, ADP1 and PGK genes
REFERENCE	Yeast 8 (5), 409-417 (1992)
TITLE	1626432
JOURNAL PUBMED AUTHORS	Oliver, S.G., van der Aart, Q.J., Agostoni-Carbone, M.L., Aigle, M.,
REFERENCE	Alberghina, L., Alexandraki, D., Antoine, G., Anwar, R., Ballesta, J.P.,
TITLE	Benit, P. et al.
JOURNAL PUBMED AUTHORS	The complete DNA sequence of yeast chromosome III
REFERENCE	Nature 357 (6373), 38-46 (1992)
TITLE	1574125
JOURNAL PUBMED AUTHORS	Wilson, C., Grisanti, P. and Frontali, L.
REFERENCE	The complete sequence of a 6146 bp fragment of Saccharomyces
TITLE	cerevisiae chromosome III contains two new open reading frames
JOURNAL PUBMED AUTHORS	Yeast 8 (7), 569-575 (1992)
REFERENCE	1523889
TITLE	10
JOURNAL PUBMED AUTHORS	Scherens, B., Messenguy, F., Gigot, D. and Dubois, E.
REFERENCE	The complete sequence of a 9,543 bp segment on the left arm of
TITLE	chromosome III reveals five open reading frames including
JOURNAL PUBMED AUTHORS	glucokinase and the protein disulfide isomerase
REFERENCE	Yeast 8 (7), 577-585 (1992)
TITLE	1523890
JOURNAL PUBMED AUTHORS	11 (bases 26740 to 32076)
REFERENCE	Defoor, E., Debrabandere, R., Keyers, B., Voet, M. and Voickaert, G.
TITLE	Nucleotide sequence of diOB, a BamHI fragment on the small-ring
JOURNAL PUBMED AUTHORS	chromosome III of Saccharomyces cerevisiae
REFERENCE	Yeast 8 (8), 681-687 (1992)
TITLE	1441748
JOURNAL PUBMED AUTHORS	12 (bases 169581 to 171116; 171683 to 172169)
REFERENCE	Agostoni Carbone, M.L., Panzeri, L., Muzi Falconi, M., Carcano, C.,
TITLE	Plevani, P. and Lucchini, G.
JOURNAL PUBMED AUTHORS	Nucleotide sequence of 9.2 kb left of CRV1 on yeast chromosome III
REFERENCE	from strain AB972: evidence for a Ty insertion and functional
TITLE	analysis of open reading frame YCR28
JOURNAL PUBMED AUTHORS	Yeast 8 (9), 805-812 (1992)
REFERENCE	1332309
TITLE	13 (bases 1 to 315338)
JOURNAL PUBMED AUTHORS	TA-repeat microsatellites are closely associated with ARS consensus
REFERENCE	sequences in yeast chromosome III
TITLE	Yeast 9 (7), 753-759 (1993)
JOURNAL PUBMED AUTHORS	8368009
REFERENCE	14 (bases 1 to 315338)
TITLE	Slonimski, P.P. and Brouillet, S.
JOURNAL PUBMED AUTHORS	A data-base of chromosome III of Saccharomyces cerevisiae
REFERENCE	Yeast 9 (9), 941-1029 (1993)
TITLE	8266725
JOURNAL PUBMED AUTHORS	15 (bases 1 to 315339)
REFERENCE	Rodriguez-Cousino, N., Lill, R., Neupert, W. and Court, D.A.
TITLE	Identification and initial characterization of the cytosolic
JOURNAL PUBMED AUTHORS	protein Ycr77p
REFERENCE	Yeast 11 (6), 581-585 (1995)
TITLE	7645349
JOURNAL PUBMED AUTHORS	16
REFERENCE	MIPS.
TITLE	Direct Submission
JOURNAL PUBMED AUTHORS	Submitted (16-MAR-1992) MIPS, D-8033 Martinried, FRG. Data
REFERENCE	collected by MIPS on behalf of the European Yeast Chromosome III
TITLE	Sequencing project
JOURNAL PUBMED AUTHORS	replaced by [13]
REFERENCE	17 (bases 1 to 314957)
TITLE	Jimenez, A.
JOURNAL PUBMED AUTHORS	Direct Submission
REFERENCE	Submitted (28-DEC-1992) MIPS, D-8033 Martinried, FRG. Data
TITLE	collected by MIPS on behalf of the European Yeast Chromosome III
JOURNAL PUBMED AUTHORS	Sequencing project. Update originating from A. Jimenez
REFERENCE	replaced by [14]
TITLE	18
JOURNAL PUBMED AUTHORS	Louis, E.J.
REFERENCE	Direct Submission
TITLE	Submitted (25-JUN-1993) MIPS, D-8033 Martinried, FRG. Data
JOURNAL PUBMED AUTHORS	collected by MIPS on behalf of the European Yeast Chromosome III

Sequencing project. Update originating from E.J. Louis
revised by [18]
19 Louis, E.J.
Direct Submission
Submitted (14-FEB-1995) MIPS, D-8033 Martinsried, FRG. Data
collected by MIPS on behalf of the European Yeast Chromosome III
Sequencing project. Update originating from E.J. Louis
Revised by [20]
20 Gromadka, R.
Direct Submission
Submitted (29-JAN-1996) R. Gromadka, Protein Biosynthesis,
Institute of Biochemistry and Biophysics, Pawinski 5A, Warsaw,
Poland, Electronic Mail Address: robert@psd.ibt.waw.pl
revised by [21]
21 (bases 1 to 316613)
MIPS.
Direct Submission
Submitted (17-JUN-2001) MIPS Yeast Genome Database, GSF -
Ingolstaedter Landstrasse 1 D-85764 Neuherberg, Germany,
mips-yeast-admgef.de
Resequencing project, achieved by the joint effort of G. Valles and
G. Volckaerts laboratories. Munich information center for protein
sequences.
On Jul 3, 2001 this sequence version replaced gi:1907116.
The contig sequence which has been released to the file server in
1992 has been subject to a resequencing project, achieved by the
joint effort of G. Valles and G. Volckaerts laboratories. The
following lines present a summary of the altered entities. The
resequenced chrIII contig is 316613 bp with GCG-check: 429 GENETIC
ENTITIES valid no longer:
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frame shift in
the nt sequence of YCL014w leads to an elongated polypeptide.) This
elongated polypeptide encoded by the current YCL014w resembles the
Bud3p polypeptide from the
EMBL-Entry (Accession: SC175801; ID: U17580, total length 1636 aa)
YCL066c, PEP Y, ORF obsolete, is not an ORF in current Chromosome
III contig.
YCR062w (YCR061w + YCR062w -> YCR061w / C.A583 + C.B120 -> C.B631),
PEP Y, ORF in identical form now C-terminal part of YCR061w.
YCR068w-a (YCR068w + YCR068w-a -> YCR068w / C.C429 + C.A145 -> C
A520). PEP Y, ORF in identical form now C-terminal part of YCR068w.
YCR103c (C.F111, former ORF in region corresponding to coord.
307255-307587(C) is obsolete, open reading frame is destroyed by
stop codon after 45 aa.
NEW GENETIC ENTITIES:
YCL26c-b (C.E193(YCL027c-a)), PEP Y, new ORF
YCL021w-a (C.C125), PEP Y, new ORF
ALTERED GENETIC ENTITIES:
YCL076w, PEP Y, peptide elongated N-terminally by 51 aa YCL074w,
PEP Y, 3 aa exchanged
YCL073c, PEP Y, 4 aa exchanged
YCL068c (C.F190->C.E260), PEP Y, peptide elongated N-terminally by
70 aa YCL065w, PEP Y, 1 aa exchanged
YCL064c, PEP Y, 3 aa exchanged
YCL061c (C.D853->C.F1096), PEP Y, peptide elongated N-terminally by
243 aa YCL051w, PEP Y, 11 aa altered, 6 aa exchanged, 1 aa
additional, 4 aa less at the C-terminus
YCL050c, PEP Y, 1 aa exchanged
YCL049c, PEP Y, 4 aa exchanged
YCL042w, PEP Y, 8 aa altered, 7 aa exchanged, 1 aa additional
YCL034w (C.A265->C.B354), PEP Y, peptide elongated N-terminally by
89 aa YCL030c, PEP Y, 1 aa exchanged
YCL028w, PEP Y, 1 aa exchanged
YCL027w, PEP Y, 3 aa exchanged
YCL026c-a, PEP Y, 8 aa altered, 7 aa exchanged, 1 aa additional
YCL025c (C.F633->C.F595), PEP Y, 7 aa exchanged, the c-terminus is
shorter by 38 aa and the last 5 aa are altered
LTR deltaCLO5, 1 nt exchange

LTR deltaCLO4, 1 nt deletion
TY2A_C, PEP Y, 1 aa exchanged
Query Match 34.1%; Score 147.4; DB 4; Length 316613;
Best Local Similarity 65.2%; Pred. No. 8.4e-35;
Matches 217; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
QY 99 AAAAAATGGTATCCCGAGAAACAGTTCCTCAGCGTAAAGGATCTGATTTGGCCAAAAGGAAGT 158
DB 61177 AAAAAATGGTATCTCAAGAAACTATCAAGCAGCGTCAAGGACCTTATTTCGACAAAACGAGAT 61118
QY 159 GTTTGTTGAGCAAGACATCTGCTTACTGTTAAAGCTACTTTGTCTACCTCTTCCA 218
DB 61117 CTTTCGTGATCCAAAACGCTACTGTCTCATATGCTCCATGCGCCCTTAACACGCTTTTGA 61058
QY 219 AGAATTTGAAGCTTCCCAAACTCAAGGCCCTTGTGTTGGAATAGATGAATAGCAATGG 278
DB 61057 AAGTTAAAGTTCCCAAGGTCCAAAGTTCTGGTTTTCGATTCGATTCGATGAGGAGG 60998
QY 279 CTCAGAGATTCAGACGCTTTTAGAAGAAATCTCGGCCAAAACCTGTACCTAACCTATA 338
DB 60997 CGCAGACATTCAGGCTGCTTATATGATTAATGCGCAAGAACCGTGCACAACTCTA 60938
QY 339 CATCAATGCGAAGCACAATTGCTGTTAAACAGCGATTTGGAAACCTTTGAAGAAAATGGCAA 398
DB 60937 TATTAATGGTAAACATATTGGAGGCAACGACGACTTGCAGGAATTGAGGGAGACTGGTGA 60878
QY 399 GTTAGCTGAAATATTCAGCCGCTATTTCATA 431
DB 60877 ATTGGAGGAATTGTTAGAACCTATTCTTGCAAA 60845

RESULT 9
CNS06J47 994 bp DNA linear STS 17-AUG-2005
LOCUS T7 end of clone AS0AA025G08 of library AS0AA from strain CLIB 533
DEFINITION AL401117
ACCESSION AL401117.1 GI:12158327
VERSION STS
KEYWORDS Saccharomyces uvarum
SOURCE Saccharomyces uvarum
ORGANISM Saccharomyces uvarum
REFERENCE Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
1 (bases 1 to 994)
AUTHORS Souciet, J., Aigle, M., Artiguenave, F., Blandin, G.,
Bollotin-Fukuhara, W., Bon, E., Brothier, P., Casaregola, S., de
Montigny, J., Dujon, B., Durrens, P., Gallardin, C., Lepingle, A.,
Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O.,
Petier, S., Saurin, W., Tekai, F., Toffano-Nioche, C.,
Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
PUBMED 11152876
REFERENCE 2 (bases 1 to 994)
AUTHORS Bon, E., Neuveglise, C., Casaregola, S., Artiguenave, F., Wincker, P.,
Aigle, M. and Durrens, P.
TITLE Genomic exploration of the hemiascomycetous yeasts: 5.
Saccharomyces bayanus var. uvarum
JOURNAL FEBS Lett. 487 (1), 37-41 (2000)
PUBMED 11152880
REFERENCE 3 (bases 1 to 994)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This STS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia

angueta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source 1..994

/organism="Saccharomyces uvarum"
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/strain="CLIB 533"
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/inference="non-experimental evidence, no additional details recorded"
/note="similar to Saccharomyces cerevisiae ORF YDR513w [TTR1 ; glutaredoxin j]"
/inference="non-experimental evidence, no additional details recorded"
/note="similar to Saccharomyces cerevisiae ORF YDR514c [strong similarity to hypothetical protein YCL036w]"

misc_feature

misc_feature

ORIGIN

Query Match 34.0%; Score 147; DB 7; Length 994;
Best Local Similarity 86.6%; Pred. No. 2.4e-34;
Matches 162; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 246 CTTTGTTGGAAATTAGATGAATGACATGCTCAGAGATTCAGAGCGCTTTAGAAGA 305
DB 1 CGTTGTTGGAAATTGACGAATGACATGCTTCAAGAAATTCAGATGCTCTCGAAGA 60
QY 306 AATCTCGGGCCAAAACCTGCTACCTACGTATACATCAATGGCAACGATTCGTGTAA 365
DB 61 AATTTTCGGCCGAGAAACCGTACCAACGTTTATATCAATGGAAACATCGGTGTAA 120
QY 366 CAGCGAATTTGGAACTTTGAAGAAAATGCGAAGTTAGCTGGAATATTGAAGCGGTATT 425
DB 121 CAGCGAATTTGGAGCTTTGAAGAAAACGTAAGTTGGCTGAATATTGAACCGGTTT 180
QY 426 TCAATAG 432
DB 181 TGAATAG 187

RESULT 10

CQ785688
LOCUS CQ785688 333 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 1 from Patent WO2004018687.
ACCESSION CQ785688
VERSION CQ785688.1 GI:45720868
KEYWORDS Saccharomyces cerevisiae (baker's yeast)
SOURCE Saccharomyces cerevisiae
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE

1 Chardonens, A. and Puzio, P.
TITLE Nucleic acid sequences encoding proteins associated with abiotic stress response
JOURNAL Patent: WO 2004018687-A 1 04-MAR-2004;
BASF Plant Science GmbH (DE)

FEATURES

source 1..333
/organism="Saccharomyces cerevisiae"
/mol_type="unassigned DNA"
/db_xref="taxon:4932"
1..333
/note="unnamed protein product; GRX1"
/codon_start=1

CDS

/protein_id="CAG17725.1"
/db_xref="GI:45720869"
/translation="MVSGETIKHVDLIAENEIFVASKTYCPYCHAALNTLEKLVKVP
RSKLVLQNDNMKEGADIOAALYEINGQRTVPNIYINGKHIGNDLQELRETELEEE
LLEPTLAN"

ORIGIN

Query Match 33.2%; Score 143.4; DB 2; Length 333;
Best Local Similarity 64.7%; Pred. No. 3.7e-33;
Matches 213; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
QY 103 ATGGTATCCAGCAAGTCTGCTCAGTAAAGGATCTGATGGCCAAAGAAAGTGTTT 162
DB 1 ATGGTATCTCAAGAAACTATCAAGCAGCTCAAGGACCTTATTGCGAAGAACGATCTTC 60
QY 163 GTTGCAAGCAACATACCTGCTTACTGTAAAGCTACTTTGTCTACCTCTTTCCAAGAA 222
DB 61 GTGCGATCCAAACGCTACTGTCATCTGCCATGCGCCCTAAACACGCTTTTGAAGAG 120
QY 223 TTGAAGCTTCCCAATCCAGGCCCTTGTGTTGGATTAGATGAAATGAGCAATGCGCTCA 282
DB 121 TTAAGAGTTCCAGGTCCAAAGTCTCTGGTTTTCGCAATTGAATGACATGAAGGAGCGCA 180
QY 283 GAGATTCAAGACGCTTTTAGAAGAAATCTCGGCGCCAAACAACTGTACTAACGTATACATC 342
DB 181 GACATTCAGGCTGCGTTATATGAGATTAAATGCGCAAGAACCGTGCACCAACATCTATAT 240
QY 343 AATGCAAGCACATTTGGTGTAAACGAGGATTTGGAAACTTTGAAGAAAATGGCAAGTTA 402
DB 241 AATGTTAAACATATTGGAGGCAACGACGACTTTGAGGAATTCGAGGAGACTGCTGAATTG 300
QY 403 GCTGAATATTGAAGCGGCTATTTCATTA 431
DB 301 GAGGAATTTGTTAGAACCTATTCTTCAAA 329

RESULT 11

CR382123_00/c

WPCOMMENT

Sequence split into 18 fragments LOCUS CR382123 Accession CR382123
Fragment Name Begin End
CR382123_00 1 110000
CR382123_01 100001 210000
CR382123_02 200001 310000
CR382123_03 300001 410000
CR382123_04 400001 510000
CR382123_05 500001 610000
CR382123_06 600001 710000
CR382123_07 700001 810000
CR382123_08 800001 910000
CR382123_09 900001 1010000
CR382123_10 1000001 1110000
CR382123_11 1100001 1210000
CR382123_12 1200001 1310000
CR382123_13 1300001 1410000
CR382123_14 1400001 1510000
CR382123_15 1500001 1610000
CR382123_16 1600001 1710000
CR382123_17 1700001 1753957

LOCUS CR382123 1753957 bp DNA linear PLN 17-APR-2005
DEFINITION Kluyveromyces lactis strain NRRL Y-1140 chromosome C of strain NRRL Y-1140 of Kluyveromyces lactis.

ACCESSION

CR382123

VERSION

CR382123.1 GI:49641331

KEYWORDS

genomic DNA.

SOURCE

Kluyveromyces lactis NRRL Y-1140

ORGANISM

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

REFERENCE

AUTHORS

1 (bases 1 to 1753957)
Dujon, B., Sherman, D., Fischer, G., Durrens, P., Casaregola, S., Lafontaine, I., De Montigny, J., Marck, C., Neuvéglise, C., Talla, E., Goffard, N., Frangeul, L., Aigle, M., Anthouard, V., Babour, A.,

RESULT	13
AX489480	
LOCUS	360 bp DNA linear PAT 16-AUG-2002
DEFINITION	Sequence 6780 from Patent WO02053728.
AX489480	
ACCESSION	
VERSION	AX489480.1 GI:22323492
KEYWORDS	.
SOURCE	Candida albicans
ORGANISM	Candida albicans Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; microsporid Saccharomycetales; Candida. 1
REFERENCE	Romer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L. Gene disruption methodologies for drug target discovery Patent: WO 02053728-A 6780 11-JUL-2002;
AUTHORS	Elitra Pharmaceuticals, Inc. (US)
TITLE	
JOURNAL	
FEATURES	Location/Qualifiers 1...360

[illegible]

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Qy 307 ATCTCGGCCCAAAAACCTGACCTTAACGTATACATCAATAGCGAAGCAACATTTGGTGTAAAC 366
Db 238 ATCACTGGTCAAGAACCGTTCCAAATGTCTTTATTGGTGTCAACATAATTTGGTGGCAAT 297
Qy 367 AGCGATTGGAACTTTGAGAAAAATGCGAAGTACCTGAATATTGAAGCCGGTATTT 426
Db 298 TCCGATGTGAAGCTTTGAAGTCTAGTGACAAATATGATGACAAATCAAAGCTGCTTTA 357
Qy 427 CAA 429
Db 358 TAA 360
RESULT 14
AX537006
LOCUS AX537006 360 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 607 from Patent WO02064766.
ACCESSION AX537006
VERSION AX537006.1 GI:25263441
KEYWORDS
SOURCE
ORGANISM Candida albicans
Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
Contreras, R.H., Eberhardt, I., Luyten, W.H. and Reekmans, R.J.
Bax-responsive genes for drug target identification in yeast and
fungi
JOURNAL Patent: WO 02064766-A 607 22-AUG-2002;
JANSSEN PHARMACEUTICA N.V. (BE)
FEATURES
source
1. .360
Location/Qualifiers
/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"
ORIGIN
Query Match 20.6%; Score 89; DB 2; Length 360;
Best Local Similarity 55.4%; Pred. No. 3.2e-16;
Matches 201; Conservative 0; Mismatches 150; Indels 12; Gaps 1;
Qy 67 AGAATATTGCTAAAGATTTTATCTACTCCAAAAATGGTATCCAGGAAACAGTTGGCT 126
Db 10 ACATTATTAAACCAAGACTATTCAATACATCAACATGGTTTCATCTCAAGTTAAGAAC 69
Qy 127 CAGCTAAAGGATCTGATTGGCCAAAGGAAGTGTGTTGGCAGCAAGACATACCTGCCCT 186
Db 70 AAGGTGCAACAATTTGATCAAAACCAACCCAGTTTTCATTGGCTTCCAAATCCTATTGTCCA 129
Qy 187 TACTGTAAAGCTACTTTGTCTACCCCTCTTCCAGAAATTTGAAGCTTCCAAATCCAGGCC 246
Db 130 TACTGTAAAGCTACCAAAAGCAC-----AATTGAAGCTATAACAAGGATGCT 177
Qy 247 CTTGTGTGGAATTTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAA 306
Db 178 TACATCTTCTGAAATTAGACGAAGTTGACGCGGTCTGAAATCCAAGAACGATTATTGGAA 237
Qy 307 ATCTCGGCCCAAAAACCTGACCTTAACGTATACATCAATAGCGAAGCAACATTTGGTGTAAAC 366
Db 238 ATCACTGGTCAAGAACCGTTCCAAATGTCTTTATTGGTGTCAACATAATTTGGTGGCAAT 297
Qy 367 AGCGATTGGAACTTTGAGAAAAATGCGAAGTACCTGAATATTGAAGCCGGTATTT 426
Db 298 TCCGATGTGAAGCTTTGAAGTCTAGTGACAAATATGATGACAAATCAAAGCTGCTTTA 357
Qy 427 CAA 429
Db 358 TAA 360

RESULT 15
CR382129 06/c
WPCOMMENT

Sequence split into 33 fragments LOCUS CR382129 Accession CR382129
Fragment Name Begin End
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CR382129_32 3200001 3272609
Continuation (7 of 33) of CR382129 from base 600001 (CR382129 Yarrowia lipolytica chromosome)
Query Match 19.4%; Score 83.8; DB 4; Length 110000;
Best Local Similarity 55.0%; Pred. No. 6e-15;
Matches 191; Conservative 0; Mismatches 147; Indels 9; Gaps 1;
Qy 83 GATTTTATCTACTCCAAAAATGGTATCCAGGAAACAGTTGCTCAGTAAAGACTTT 142
Db 95727 GAGCTTTCTCTACAAACCATGGCCACCGAGTCCGCTATCAAGACCATCAAGGAGCACA 95668
Qy 143 TTGGCCAAAGGAGTGTGTTGTGACCAAGACATACCTGCCCTTACTGTAAAGCTACTT 202
Db 95667 TTGCCAAGGACAAAGGTCTTCGTGGCCCTCCAAAGTCTTACTGCCCTTACTGCAAGACACCA 95608
Qy 203 TGTCTACCCCTTCTCCAAAGAATTGAAGCTTCCCAAAATCCCAAGGCCCTTGTGTGGAATTAG 262
Db 95607 AGCAGCTGTCTTCCCAAGTTCAGGAGG-----CCAAGCCGCGTATTCGAGCTCG 95557
Qy 263 ATGAAATAGCAATATGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCGGGCCAAAAAA 322
Db 95556 ACAGCTGTACGATGTGCGGAGCTCCAGGCTGCTCTCGCCGAGATCACTTGGCCAGCGAA 95497
Qy 323 CTGTACTTAACGTATACATCAATGGCAAGCACATTTGGTGTACACGATTTTGGAACTT 382
Db 95496 CCGTTCCTCAACGTTTTCATTTGGAGGGCCAGCACATTTGGTGCAACTCCGATCTCGAGGTT 95437
Qy 383 TGAAGAAAAATGGCAAGTGTAGCTGAAATATTGAAGCCGGTATTTCAA 429
Db 95436 TTGCCCAAGAGGACGAGCTGGCCGATAGATCAAGGCTGCCCTTTAA 95390

Search completed: November 7, 2006, 04:29:46
Job time : 3046 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2006, 19:18:05 ; Search time 187 Seconds
(without alignments)
354.223 Million cell updates/sec

Title: US-10-523-362-4

Perfect score: 714

Sequence: 1 METNFSFDSNLIIVIIITLF.....DLETLKKGKLABILKPVFQ 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:*

- 1: /EMC Celerra_SID83/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
- 2: /EMC Celerra_SID83/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
- 3: /EMC Celerra_SID83/ptodata/2/pubpaa/US09_PUBCOMB.pcp.*
- 4: /EMC Celerra_SID83/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
- 5: /EMC Celerra_SID83/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
- 6: /EMC Celerra_SID83/ptodata/2/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	714	100.0	143	4	US-10-451-467A-134
2	714	100.0	143	5	US-10-523-362-4
3	391	54.8	110	4	US-10-451-467A-66
4	391	54.8	110	5	US-10-523-362-2
5	300.5	42.1	119	4	US-10-032-585-7780
6	300.5	42.1	119	4	US-10-451-467A-608
7	230.5	32.0	135	4	US-10-767-701-42668
8	228.5	32.0	135	4	US-10-425-115-229411
9	228.5	32.0	135	4	US-10-425-115-229409
10	225	31.5	104	4	US-10-425-115-362857
11	219	30.7	101	4	US-10-767-701-51857
12	218.5	30.6	131	6	US-11-096-568A-26784
13	216.5	30.3	129	4	US-10-425-115-352583
14	216.5	30.3	129	4	US-10-425-115-229162
15	216	30.3	169	4	US-10-424-599-239954
16	216	30.3	136	4	US-10-437-963-149594
17	215.5	30.2	136	5	US-10-523-362-46
18	215	30.2	127	5	US-10-523-362-18
19	215	30.1	102	4	US-10-425-115-352583
20	215	30.1	113	6	US-11-096-568A-26785
21	214.5	30.0	135	5	US-10-523-362-32
22	214.5	30.0	133	5	US-10-523-362-22
23	209	29.3	112	4	US-10-424-599-239952
24	208	29.1	134	4	US-10-437-963-131826
25	207.5	29.1	173	5	US-10-424-599-239955
26	206	28.9	102	4	US-10-523-362-20
27	206	28.9	111	5	US-10-425-115-331215
28	206	28.9	111	5	US-10-523-362-28

28	205.5	28.8	128	4	US-10-767-701-43209	Sequence 43209, A
29	205	28.7	97	4	US-10-425-115-312491	Sequence 312491, A
30	204	28.6	98	4	US-10-425-115-334023	Sequence 334023, A
31	204	28.6	120	5	US-10-523-362-16	Sequence 16, Appl
32	199	27.9	129	4	US-10-424-599-175134	Sequence 175134, A
33	199	27.9	179	5	US-10-523-362-34	Sequence 34, Appl
34	198	27.7	111	5	US-10-523-362-18	Sequence 26, Appl
35	197	27.6	136	5	US-10-523-362-18	Sequence 18, Appl
36	196.5	27.5	116	6	US-11-097-143-17640	Sequence 17640, A
37	196	27.5	130	5	US-10-523-362-30	Sequence 30, Appl
38	194	27.2	127	4	US-10-451-467A-598	Sequence 598, App
39	189	26.5	114	6	US-11-097-143-15012	Sequence 15012, A
40	185.5	26.0	131	4	US-10-437-963-154842	Sequence 154842, A
41	184.5	25.8	166	4	US-10-424-599-159065	Sequence 159065, A
42	184.5	25.8	177	4	US-10-425-115-201600	Sequence 201600, A
43	184	25.8	164	4	US-10-424-599-175133	Sequence 175133, A
44	183	25.6	105	4	US-10-425-115-308251	Sequence 308251, A
45	181	25.4	107	4	US-10-424-599-146193	Sequence 146193, A

ALIGNMENTS

RESULT 1

US-10-451-467A-134

; Sequence 134, Application US/10451467A

; Publication No. US20040161840A1

; GENERAL INFORMATION:

; APPLICANT: CONTRERAS, ROLAND HENRI

; APPLICANT: EBERHARDT, INES

; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS

; APPLICANT: REEKMAN, RIEKA JOSEPHINA

; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN

; TITLE OF INVENTION: YEAST AND FUNGI

; FILE REFERENCE: JAB-1667

; CURRENT APPLICATION NUMBER: US/10/451,467A

; CURRENT FILING DATE: 2003-06-19

; PRIOR APPLICATION NUMBER: EP 00870318.3

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: EP 01870002.1

; PRIOR FILING DATE: 2001-01-04

; PRIOR APPLICATION NUMBER: EP 01870003.9

; PRIOR FILING DATE: 2001-01-09

; NUMBER OF SEQ ID NOS: 732

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 134

; LENGTH: 143

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

US-10-451-467A-134

Query Match 100.0%; Score 714; DB 4; Length 143;

Best Local Similarity 100.0%; Pred. No. 9.7e-69; Indels 0; Gaps 0;

Matches 143; Conservative 0; Mismatches 0;

QY 1 METNFSFDSNLIIVIIITLFATRIIAKRFLSPKMSQETVAHVKDLIGQKEVFVAAKTY 60

DB 1 METNFSFDSNLIIVIIITLFATRIIAKRFLSPKMSQETVAHVKDLIGQKEVFVAAKTY 60

QY 61 CPYCKATLSTLFOELNVPKSKALVLELDEMSNGSEIQTDALEELISGQKTPVNVINGKHIG 120

DB 61 CPYCKATLSTLFOELNVPKSKALVLELDEMSNGSEIQTDALEELISGQKTPVNVINGKHIG 120

QY 121 GNSDLETLKKGKLABILKPVFQ 143

DB 121 GNSDLETLKKGKLABILKPVFQ 143

RESULT 2

US-10-523-362-4

; Sequence 4, Application US/10523362

; Publication No. US20060064784A1

; GENERAL INFORMATION:

APPLICANT: Chardonens, Agnes
APPLICANT: Puzio, Piotr
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Proteins Associated with Abiotic
FILE REFERENCE: 532622010300
CURRENT FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 143
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-523-362-4

Query Match 100.0%; Score 714; DB 5; Length 143;
Best Local Similarity 100.0%; Pred. No. 9.7e-69;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFSFDSNLIVIIITLPTATRIIAKRFLSTPKMVSOETVAHVXKDLIGQKEVFVAAKTY 60
DB 1 METNFSFDSNLIVIIITLPTATRIIAKRFLSTPKMVSOETVAHVXKDLIGQKEVFVAAKTY 60
QY 61 CPYCKATLSTLFOELNVPKSKALVLEDEMSNGSEIQDALEESGQKTVPNVYNGKHG 120
DB 61 CPYCKATLSTLFOELNVPKSKALVLEDEMSNGSEIQDALEESGQKTVPNVYNGKHG 120
QY 121 GNSDLETLLKNGKLAELKPVFQ 143
DB 121 GNSDLETLLKNGKLAELKPVFQ 143

RESULT 3
US-10-451-467A-66
Sequence 66, Application US/10451467A
Publication No. US20040161840A1
GENERAL INFORMATION:
APPLICANT: CONTRERAS, ROLAND HENRI
APPLICANT: EBERHARDT, INES
APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKMAN, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: EP 00870318.3
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66
LENGTH: 110
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-66

Query Match 54.8%; Score 391; DB 4; Length 110;
Best Local Similarity 64.5%; Pred. No. 4.9e-34;
Matches 69; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

QY 35 MVSOETVAHVXKDLIGQKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLEDEMSNGS 94
DB 1 MVSOETIKHVXKDLIAENEIFVASKTYCPYCHAAALNTLFEKLVPRSKVLVLQNDMKEGA 60
QY 95 EIQDALEESGQKTVPNVYNGKHGNSDLETLLKNGKLAELKPV 141
DB 61 DIQAALYEINGQRTVPNIYNGKHGNSDLETLLKNGKLAELKPV 107

RESULT 4
US-10-523-362-2
Sequence 2, Application US/10523362
Publication No. US20060064784A1
GENERAL INFORMATION:
APPLICANT: Chardonens, Agnes
APPLICANT: Puzio, Piotr
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Proteins Associated with Abiotic
FILE REFERENCE: 532622010300
CURRENT FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 110
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-523-362-2

Query Match 54.8%; Score 391; DB 5; Length 110;
Best Local Similarity 64.5%; Pred. No. 4.9e-34;
Matches 69; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

QY 35 MVSOETVAHVXKDLIGQKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLEDEMSNGS 94
DB 1 MVSOETIKHVXKDLIAENEIFVASKTYCPYCHAAALNTLFEKLVPRSKVLVLQNDMKEGA 60
QY 95 EIQDALEESGQKTVPNVYNGKHGNSDLETLLKNGKLAELKPV 141
DB 61 DIQAALYEINGQRTVPNIYNGKHGNSDLETLLKNGKLAELKPV 107

RESULT 5
US-10-032-585-7780
Sequence 7780, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10192-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7780
LENGTH: 119
TYPE: PRT
ORGANISM: Candida albicans
US-10-032-585-7780

Query Match 42.1%; Score 300.5; DB 4; Length 119;
Best Local Similarity 50.4%; Pred. No. 3.2e-24;
Matches 61; Conservative 24; Mismatches 31; Indels 5; Gaps 2;

QY 19 LPATRIIAKRFLSTPKMVSOETVAHVXKDLIGQKEVFVAAKTYCPYCKATLSTLFOELNVP 78
DB 1 MPRT-LLTAKLNTSTMTVSSQVKNKVEQLIKTPVFIASKSYCPYCKATKST----IEAI 55
QY 79 KSKALVLEDEMSNGSEIQDALEESGQKTVPNVYNGKHGNSDLETLLKNGKLAEL 138
DB 56 TKDAVILELDEVDGAEIQALLETGQRTVPNVFIQGHIGNSDVQALKSSDKLDDKI 115
QY 139 K 139
DB 116 K 116

RESULT 6
US-10-451-467A-608

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; Sequence 608, Application US/10451467A
; Publication No. US20040161840A1
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MAR
; APPLICANT: REEKMAN, RIENKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GEN
; TITLE OF INVENTION: YEAST AND FUNGI
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: EP 00870318
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: EP 01870002
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870003
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 732
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 608
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-451-467A-608

```

	Query Match	42.1%;	Score	300.5;	DB	4;	Length	119;
	Best Local Similarity	50.4%;	Pred.	No. 3.2e-24;				
	Matches	61;	Conservative	24;	Mismatches	31;	Indels	5; Gaps 2;
QY	19	LPAATRIIAKFLSPKMNVSQETVAHVHVDLIGQEVFAAKTYCPCYCATLTSLTFQLNVP	78					
Db	1	MFRT-LTTRKLFTNTVSSQVKNVQLIKTPVFIAASKYCPCYCATKST----	1EAI	55				
QY	79	KSKALVLDELDEMSGISIQDABEISGQKTVPNVYINGKHIGGNSDLDTLKNGKLAAIL	138					
Db	56	TKDAYILELDEVDDGAIIQIALLLEITQTQRTVPNVFVGQHIGGNSDVQALKSSDKLDKI	115					
QY	139	K	139					
Db	116	K	116					

```

RESULT 7
US-10-767-701-42668
; Sequence 42668, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 42668
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C8825_1.pep
US-10-767-701-42668

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Query Match      32.3%; Score 230.5; DB 4; Length 135;
Best Local Similarity 42.6%; Pred.No. 1.4e-16;
Matches 46; Conservative 26; Mismatches 27; Indels 9; Gaps 3;

ΩY 31 STPKMSQETVAHKVHKKILIGQKEVFVAARTCPYCCKATLSTLFQELNVPKSKALVLEDEM 90
                                     :|::|||:
Db 29 SSKP-----SFVKSTVSADHDVVIFSKSYCPCYCKRA-KAVFKELQL-KIEPYVELLDQR 79
                                     :|::|||:
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Qy	91	SN	GS	IO	DA	LE	IS	OK	TP	PN	YI	NG	KH	TG	NS	DL	ET	LK	KG	KL	AE	TL	130

```

Query Match      32.0%; Score 228.5; DB 4; Length 135;
Best Local Similarity 43.5%; Pred. No. 2.3e-16;
Matches 47; Conservative 24; Mismatches 28; Indels 9; Gaps 3;

Qy 31 STPWSQETVAHVHKLIGQKEVFVAAKTVCPCYKATLSTLFQELNVPKSKALVLEDEM 90
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 29 SSPK-----SFVKSTVAHDVVFISKSYCPYCKRA-KAVFKELEL-KKEPYVVELDQR 79

Qy 91 SNGSETQDALEETSGQKTPVNVYINGKHIGCNSDLETLKNGKLAETL 138
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 80 EDGSETQDALEETVGRTVPQVFPVGHKLGSGDDTVDVSYESGKLARLT 127

```

```

RESULT 9
US-10-425-115-229409
; Sequence 229409, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 229409
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_140813C.1.pep
US-10-425-115-229409

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Query Match	32.0%	Score 228.5;	DB 4;	Length 153;
Best Local Similarity	43.5%;	Pred. No. 2.7e-16;		
Matches	47;	Conservative	28;	Indels 9; Gaps 3;
Qy	31	STPRWSQETVAHVKDLIGQKVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLEIDEM	90	
		: : : : : : :		
Db	47	SSPK-----SFVKTSVAHDVVFPSKYCPYCKKA-KAVFKELEL-KKEPYVVELDQR	97	
Qy	91	SNSGEIQDALEEISGQKTVPNVINGKHIGNSDLETLKGNGKLAETL	138	


```

Db      13  AAALIALAALGNAAGSTASKSPFKVSTKVAHDVWIFSKSYCPYCRRA-KAVFKELEL-KK 70
Qy      81  KALVLELDMSGNSHFIQDALEISQCKTVPNVYINGKHIGNSDLETLKQCKLAEIL 138
Db      71  EPYVVELDQREDEWEIQDALSMDVGRRTVPQVFVHGKHLGMSDDTVEAYESGKLAKLL 128

Search completed: November 6, 2006, 19:22:04
Job time : 188 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 6, 2006, 19:12:20 ; Search time 41 Seconds
(without alignments)
335.585 Million cell updates/sec

Title: US-10-523-362-4

Perfect score: 714

Sequence: 1 METNFSFDSNLIVIIITLF.....DLETLKNGKLAILKPVFQ 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	714	100.0	143	1 GDBY	glutaredoxin - yea
2	391	54.8	110	1 S19363	glutaredoxin GRX1
3	224	31.4	109	2 T48748	probable glutaredoxin
4	212	29.7	101	2 T38824	thioltransferase -
5	209	29.3	112	2 JCS445	glutaredoxin - ric
6	203	28.4	102	2 S54825	glutaredoxin - cas
7	199	27.9	179	2 B84587	probable glutaredoxin
8	196	27.5	130	2 G96802	probable glutaredoxin
9	194	27.2	134	2 T12219	glutaredoxin I - c
10	178	24.9	110	2 T37724	probable thioltran
11	154	21.6	149	2 T16026	hypothetical prote
12	151.5	21.2	105	1 GDPG	glutaredoxin - pig
13	151.5	21.2	203	1 S45869	glutaredoxin homol
14	147.5	20.7	105	1 GDBO	glutaredoxin - bov
15	146	20.4	102	2 B71422	probable glutaredoxin
16	143	20.0	106	1 S47472	glutaredoxin - hum
17	143	20.0	231	1 S52509	probable membrane
18	142	19.9	176	2 T04526	hypothetical prote
19	141.5	19.8	106	1 GDRB	glutaredoxin - rab
20	140	19.6	102	2 H71421	probable glutaredoxin
21	136	19.0	102	2 F71421	probable glutaredoxin
22	136	19.0	102	2 A71422	probable glutaredoxin
23	136	19.0	102	2 G71421	probable glutaredoxin
24	136	19.0	102	2 H86160	hypothetical prote
25	131	18.3	102	2 T48082	glutaredoxin-like
26	125.5	17.6	92	2 AC3275	glutaredoxin [impo
27	124.5	17.4	103	2 T48084	glutaredoxin-like
28	124.5	17.4	108	1 E42510	glutaredoxin 1 - v
29	124	17.4	107	2 AE1906	hypothetical prote

ALIGNMENTS

RESULT 1

GDBY

Glutaredoxin - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein YDR513w; thioltransferase

C;Species: Saccharomyces cerevisiae

C;Date: 31-Dec-1990 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S69570; JQ1612; A35492

R;Dietrich, F.S.

submitted to the EMBL Data Library, August 1995

A;Description: The sequence of S. cerevisiae cosmids 8166, 9787, 9717, and lambda 3073.

A;Reference number: S69553

A;Accession: S69570

A;Molecule type: DNA

A;Residues: 1-143 <DIE>

A;Cross-references: UNIPROT:P17695; UNIPARC:UPI000004F902; EMBL:U33057; NID:g927764; PID:

R;Gan, Z.R.

Biochem. Biophys. Res. Commun. 187, 949-955, 1992

A;Title: Cloning and sequencing of a gene encoding yeast thioltransferase.

A;Reference number: JQ1612; MUID:92412147; PMID:1530649

A;Accession: JQ1612

A;Molecule type: DNA

A;Residues: 35-143 <GAN>

A;Cross-references: UNIPARC:UPI0000168989; GB:S45268; NID:g256162; PIDN:AAB23389.1; PID:

A;Experimental source: strain DMV6

R;Gan, Z.R.; Polokoff, M.A.; Jacobs, J.W.; Sardana, M.K.

Biochem. Biophys. Res. Commun. 188, 944-951, 1990

A;Title: Complete amino acid sequence of yeast thioltransferase (glutaredoxin).

A;Reference number: A35492; MUID:90267489; PMID:2189409

A;Accession: A35492

A;Molecule type: protein

A;Residues: 36-141 <GA2>

A;Cross-references: UNIPARC:UPI0000171E32

C;Genetics:

A;Gene: SGD:TTR1; GRX2; MIPS:YDR513W

A;Map position: 4R

C;Function:

A;Description: thioltransferase catalyzes cellular thiol-disulfide transhydrogenation re

C;Superfamily: glutaredoxin; glutaredoxin homology

C;Keywords: acetylated amino end; cytosol; electron transfer; redox-active disulfide

F;36-141/Product: glutaredoxin #status experimental <MAT>

F;43-138/Domain: glutaredoxin homology <GLUT>

F;36/Modified site: acetylated amino end (Val) (in mature form) #status experimental

F;61-64/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 714; DB 1; Length 143;

Best Local Similarity 100.0%; Pred. No. 6.8e-56;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METNFSFDSNLIVIIITLFPATRIIAKRFILSTPKMVSQETVAHVHVDLIGQKEVFVAAKTY 60

Db 1 METNFSFDSNLIVIIITLFPATRIIAKRFILSTPKMVSQETVAHVHVDLIGQKEVFVAAKTY 60

QY 61 CPYCKATLSTLFOELNVPKSKALVLELDMSGSEIOTDALEEEISGQKTVPNVYNGKHIG 120
DB 61 CPYCKATLSTLFOELNVPKSKALVLELDMSGSEIQDALEEEISGQKTVPNVYNGKHIG 120
QY 121 GNSDLETLKNGKLAELIKPVFQ 143
DB 121 GNSDLETLKNGKLAELIKPVFQ 143

RESULT 2

S19363
N;Alternate names: GRX1 - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: S19363
R;Hollenberg, C.P.; Kleinhaus, U.; Lutzenkirchen, K.; Ramezani Rad, M.; Xu, G.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19350
A;Accession: S19363
A;Molecule type: DNA
A;Residues: 1-110 <HOL>
A;Cross-references: UNIPROT:P25373; UNIPARC:UPI000004F8E0; EMBL:X59720; NID:g19071116; P1
C;Genetics:
A;Gene: GRX1
A;Cross-references: SGD:S0000540; MIPS:YCL035C
A;Map position: 3L
C;Function:
A;Description: thioltransferase catalyzes cellular thiol-disulfide transhydrogenation re
C;Superfamily: glutaredoxin; glutaredoxin homology
C;Keywords: electron transfer; redox-active disulfide
F;9-104/Domain: glutaredoxin homology <GLUT>
F;27-30/Disulfide bonds: redox-active #status predicted

Query Match 54.8%; Score 391; DB 1; Length 110;
Best Local Similarity 64.5%; Pred. No. 1.5e-27;
Matches 69; Conservative 23; Mismatches 15; Indels 0; Gaps 0;
QY 35 MVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLELDMSG 94
DB 1 MVSQETIKHVKDLIAENEIVASKTYCPYCHAAINTLFEKLKVPKSKVLVLQNDMKEGA 60
QY 95 EIQDALEEEISGQKTVPNVYNGKHIGNSDLETLKNGKLAELIKPV 141
DB 61 DIQAALYEINGQRTVPVNYINGKHIGGNDLQELRETGELELEPI 107

RESULT 3

T48748
probable glutaredoxin 8D4.220 [similarity] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: T48748
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24541
A;Accession: T48748
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <SCH>
A;Cross-references: UNIPROT:Q99718; UNIPARC:UPI000006A1A0; EMBL:AL353819; GSPDB:GN00112;
A;Experimental source: cosmid contig 8D4; strain 74
C;Genetics:
A;Gene: NCSP:8D4.220
A;Map position: 2
A;Introns: 19/1
C;Superfamily: glutaredoxin; glutaredoxin homology
C;Keywords: electron transfer; redox-active disulfide
F;26-29/Disulfide bonds: redox-active #status predicted

Query Match 31.4%; Score 224; DB 2; Length 109;
Best Local Similarity 42.6%; Pred. No. 8.2e-13;

Matches 46; Conservative 22; Mismatches 36; Indels 4; Gaps 1;
QY 36 VSOETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLELDMSGSE 95
DB 1 MSDAAQTAKAQQLINDNAVVFVFSKYCPYCSNFK----QILDGLNAKYATYELNQESDGS 56
QY 96 IODALEEEISGQKTVPNVYNGKHIGNSDLETLKNGKLAELIKPVFQ 143
DB 57 VQDALLKLTGQRTVPVNYINGKHIGNSDLEAVVKNKNGKGIQELLQ 104

RESULT 4

T38824
thioltransferase - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: glutaredoxin
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38824; T43362; T50489
R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21813
A;Accession: T38824
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-101 <CON>
A;Cross-references: UNIPROT:O36032; UNIPARC:UPI000012B7C0; EMBL:Z98980; PIDN:CAB11722.1;
R;Kawamukai, M.
submitted to the EMBL Data Library, June 1998
A;Description: S.pombe glutaredoxin.
A;Reference number: Z22451
A;Accession: T43362
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-101 <KAW>
A;Cross-references: UNIPARC:UPI000012B7C0; EMBL:AB015167; PIDN:BAA28750.1
R;Kim, H.G.; Cho, Y.W.; Park, E.H.; Lim, C.J.
submitted to the EMBL Data Library, January 1999
A;Description: Characterization of cDNA encoding thioltransferase (glutaredoxin) from Sci

A;Reference number: Z25091
A;Accession: T50489
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-101 <KIM>
A;Cross-references: UNIPARC:UPI000012B7C0; EMBL:AF121275; PIDN:AAD25391.1
C;Genetics:
A;Gene: grx1; SPAC4F10.20
A;Map position: 1
A;Introns: 7/3; 25/2; 58/1
C;Superfamily: glutaredoxin; glutaredoxin homology
C;Keywords: electron transfer; redox-active disulfide
F;25-28/Disulfide bonds: redox-active #status predicted

Query Match 29.7%; Score 212; DB 2; Length 101;
Best Local Similarity 46.2%; Pred. No. 8.6e-12;
Matches 42; Conservative 17; Mismatches 28; Indels 4; Gaps 1;

QY 44 VKDLIGQKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLELDMSGSEIQDALEEI 103
DB 8 VDSAVADNDVVVFAKSYCPYCHATEKVIADK----KIKAAQVYQIDLMNNGDRIQSYLLKK 63
QY 104 SQQKTVPNVYNGKHIGNSDLETLKNGK 134
DB 64 TQRTVPVNYINGKHIGVGGNSDFQALFKK 94

RESULT 5

JC5445
glutaredoxin - rice
N;Alternate names: thioltransferase
C;Species: Oryza sativa (rice)
C;Date: 10-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: JC5445; PC4325; S41736

R;Sha, S.; Minakuchi, K.; Higaki, N.; Sato, K.; Ohtsuki, K.; Kurata, A.; Yoshikawa, H.; J. Biochem. 121, 842-848, 1997

A;Title: Purification and characterization of glutaredoxin (chiolttransferase) from rice

A;Reference number: JC5445; MUID:97335928; PMID:9192723

A;Accession: JC5445

A;Molecule type: mRNA

A;Residues: 1-112 <SHA1>

A;Cross-references: UNIPROT:P55142; UNIPARC:UPI000016DEAF

A;Accession: PC4325

A;Molecule type: protein

A;Residues: 2-5;8-106 <SHA2>

A;Cross-references: UNIPARC:UPI0000174DF0; UNIPARC:UPI0000174DF1

A;Experimental source: strain L. cv. Nipponbare

R;Minakuchi, K.; Yabushita, T.; Masumura, T.; Ichihara, K.; Tanaka, K. FEBS Lett. 337, 157-160, 1994

A;Title: Cloning and sequence analysis of a cDNA encoding rice glutaredoxin.

A;Reference number: S41736; MUID:94116670; PMID:8287970

A;Accession: S41736

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-33; 'G', 35-112 <MIN>

A;Cross-references: UNIPARC:UPI000012B7D4; GB:X77150; NID:g485952; PIDN:CAA54397.1; PID: C;Superfamily: Glutaredoxin; Glutaredoxin homology

C;Keywords: blocked amino end; electron transfer; redox-active disulfide

F;2-106/Product: glutaredoxin #status experimental <MAT>

F;5-96/Domain: glutaredoxin homology <GLUT>

F;2/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #status

F;23-26/Disulfide bonds: redox-active #status predicted

Query Match 29.3%; Score 209; DB 2; Length 112;
Best Local Similarity 44.9%; Pred. No. 1.8e-11;
Matches 44; Conservative 17; Mismatches 33; Indels 4; Gaps 2;

Qy 41 VAHVKDLIGQKEVFAAKTCYPCYKATLSTLTFQELNVPKSKALVLELDMSGSEIOTAL 100
Db 3 LAKAKETVAGPVVVSYSKCPFC-VRVKLFPQLG---ATFKAIEDLGSSELSQSL 58

Qy 101 BEISGQKTPNVYINGKHGNSDLETLKNGKLAEL 138
Db 59 AEWTGQRTVNVFNGKHIGGCDTTLANNKGLVPLL 96

RESULT 6

S54825

C;Species: Ricinus communis (castor bean)

C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: S54825

R;Szederkenyi, J.; Schobert, C.
submitted to the EMBL Data Library, May 1995

A;Description: cDNA expressed in Ricinus cotyledons.

A;Reference number: S54825

A;Accession: S54825

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-102 <SZE>

A;Cross-references: UNIPROT:P55143; UNIPARC:UPI000012B7D9; EMBL:Z49699

C;Superfamily: glutaredoxin; glutaredoxin homology

C;Keywords: electron transfer; redox-active disulfide

F;5-96/Domain: glutaredoxin homology <GLUT>

F;23-26/Disulfide bonds: redox-active #status predicted

Query Match 28.4%; Score 203; DB 2; Length 102;
Best Local Similarity 46.8%; Pred. No. 5.4e-11;
Matches 44; Conservative 14; Mismatches 32; Indels 4; Gaps 2;

Qy 45 KDLIGQKEVFAAKTCYPCYKATLSTLTFQELNVPKSKALVLELDMSGSEIOTALBEIS 104
Db 7 KELVSSNAVVFSTKYCPYC-TSVKLLDQLG---AKYKVELDTSDEIQTALAEWT 62

Qy 105 GQRTVPNVYINGKHGNSDLETLKNGKLAEL 138
Db 63 GQRTVPNVFNGKHIGGCDSTTAKHSQQLVPLL 96

RESULT 7

B84587

Probable glutaredoxin [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: B84587

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: B84587

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-179 <STO>

A;Cross-references: UNIPROT:Q9SK75; UNIPARC:UPI00000A28C9; GB:AE002093; NID:g4512708; PID: C;Genetics:

A;Gene: At2g20270

A;Map position: 2

Query Match 27.9%; Score 199; DB 2; Length 179;
Best Local Similarity 41.5%; Pred. No. 2.3e-10;
Matches 49; Conservative 24; Mismatches 39; Indels 6; Gaps 4;

Qy 23 RIATKRFSLTPKMSQETVAH-VKDLIGQKEVFAAKTCYPCYKATLSTLTFQELNVPKSK 81
Db 56 RCSSVKAMSSSSSGSTLEETVKTVAENPVVYSKTCWY-SSQVKSFLKSLQV---E 111

Qy 82 ALVLEIDEM-SNGSETQDALEIEISGQKTPNVYINGKHGNSDLETLKNGKLAEL 138
Db 112 PLVVELDQLGSEGSQLVLEKITQYTPNVFNGKHIGGCDSTLQLHNGKEAL 169

RESULT 8

G96802

Probable glutaredoxin [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004

C;Accession: G96802

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: G96802

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-130 <STO>

A;Cross-references: UNIPROT:Q9FVX1; UNIPARC:UPI000009E782; GB:AE005173; NID:g11079490; PID: C;Genetics:

A;Gene: F2p24.8

A;Map position: 1

C;Superfamily: glutaredoxin

Query Match 27.5%; Score 196; DB 2; Length 130;
Best Local Similarity 33.9%; Pred. No. 2.9e-10;
Matches 43; Conservative 30; Mismatches 46; Indels 8; Gaps 3;

Qy 12 IVIITITLPATRIAKRFSLTPKMSQETVAHVKDLIGQKEVFAAKTCYPCYKATLSTL 71
Db 9 VVVAALLP-----VVLCDLSNSAGANSVSFAFQNALSNKIVIFSICYCLRS-KRI 63

Qy 72 FOELNVPKSKALVLELDMSGSEIOTALBEISGQKTPNVYINGKHGNSDLETLKKN 131
Db 1

C;Superfamily: glutaredoxin; glutaredoxin homology
C;Keywords: acetylated amino end; deoxyribonucleotide biosynthesis; electron transfer; r
F;4-98/Domain: glutaredoxin homology <GLUT>
F;1/Modified site: acetylated amino end (Ala) #status experimental
F;22-25/Disulfide bonds: redox-active #status predicted
F;76-82/Disulfide bonds: #status predicted

Query Match 20.7%; Score 147.5; DB 1; Length 105;
Best Local Similarity 37.0%; Pred. No. 4.4e-06;
Matches 37; Conservative 19; Mismatches 39; Indels 5; Gaps 2;

QY 42 AHVKDLIGQKEVFVAAKTCYPYCKATLTLFQELNVPKSKALV--LELDEMNGSEIQDA 99
DB 3 AFVNSKIQPKGVVFIKPTCPYCKATQELLSQ---LPPKQGLLEFVDITAAAGNISEIQDY 59
QY 100 LEESGQKTPVNNVYINGKHIGGNSDLETLKXGKLAELK 139
DB 60 LQQLTGARTVPRVFIGQECIGGTDLVNMHGERGELLTRLK 99

RESULT 15
B71422
Probable glutaredoxin - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C;Accession: B71422
P.;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirke
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giele
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech,
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Auer
C.; Chaiwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thali
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: B71422
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-102 <BEV>
A;Cross-references: UNIPROT:O23421; UNIPARC:UPI000009FB5C; GB:Z97339; NID:G2244901; PID:G
C;Genetics:
A;Map position: 4COP9-4G3845
C;Superfamily: glutaredoxin; glutaredoxin homology
C;Keywords: deoxyribonucleotide biosynthesis; electron transfer
F;3-94/Domain: glutaredoxin homology <GLUT>

Query Match 20.4%; Score 146; DB 2; Length 102;
Best Local Similarity 35.7%; Pred. No. 5.7e-06;
Matches 35; Conservative 22; Mismatches 35; Indels 6; Gaps 3;

QY 43 HVKDLIGQKEVFVAAKTCYPYCKA--TLSTLQELNVPKSKALVLELDEMNGSEIQDALE 101
DB 3 NLQKMISEKSVIFSKNSC--CMSTYIKTLFDLGV---NPTIYELDEISRKGIEHALA 57
QY 102 EISGQKTPVNNVYINGKHIGGNSDLETLKXGKLAELK 139
DB 58 QLGCSPVPPVFIGQLVGGANQVMSLHLSRSLVPMLK 95

Search completed: November 6, 2006, 19:17:52
Job time : 42 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 6, 2006, 19:08:49 ; Search time 301 Seconds
(without alignments)
439.459 Million cell updates/sec

Title: US-10-523-362-4

Perfect score: 714

Sequence: 1 METNFGDSNLIVIIITLF.....DLFTLKNKGKLAILKPVFQ 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	714	100.0	143	1	GLRX2 YEAST
2	391	54.8	110	1	GLRX1 YEAST
3	333	46.6	107	2	O6CUV6 KLUJLA
4	306.5	42.9	111	2	O751W5 ASHGO
5	300.5	42.1	119	2	Q5ABH1 CANAL
6	276	38.7	104	2	O6BIM4 DEBHA
7	271.5	38.0	105	2	O6CCV8 YARLI
8	263	36.8	106	2	O4IL11 GIBZE
9	253.5	35.5	156	2	O3MPD5 CANAL
10	233.5	35.5	156	2	Q5AH29 CANAL
11	238.5	33.4	102	2	O5B5G5 EMENI
12	232	32.5	113	2	O6BT54 DEBHA
13	230.5	32.3	102	2	O2UJ38 ASPOR
14	224	31.4	109	2	O9P718 NEUCR
15	217	30.4	139	2	O8S311 PROSI
16	216	30.3	136	2	O67U24 ORYSA
17	215	30.1	135	2	Q9M457 ARATH
18	212	29.7	101	1	GLRX1 SCHPO
19	212	29.7	102	2	O4P415 USTWA
20	212	29.7	102	2	O4WJG1 ASPFU
21	211	29.6	596	2	O66J56 XENLA
22	210	29.4	135	2	Q8LF06 ARATH
23	209	29.3	112	1	GLRX ORYSA
24	209	29.3	112	2	O7FA28 ORYSA
25	208	29.1	113	2	Q94J59 DESAN
26	207	29.0	113	2	O7XY25 WHEAT
27	207	29.0	600	2	O7T2C8 BRACHYD
28	206	28.9	111	2	Q9FNE2 ARATH
29	203.5	28.5	125	2	Q8L8T2 ARATH
30	203	28.4	102	1	GLRX RICCO
31	201	28.2	115	2	Q945T3 TILPL

081187 vernicia fo
Q55Tf6 cryptococcu
Q9SK75 arabidopsis
Q8RXH1 arabidopsis
Q50042 fritillaria
Q9FM49 arabidopsis
Q7YU08 aphelenchus
Q9W2D1 drosophila
O6DH06 brachydanio
Q8LBS4 arabidopsis
Q5AH28 candida alb
Q3MPD6 CANAL
O65169 mesembryant

ALIGNMENTS

RESULT 1

GLRX2 YEAST
ID GLRX2 YEAST STANDARD; PRT; 143 AA.
AC P17695; Q6B234;
DT 01-AUG-1990, integrated into UniProtKB/Swiss-Prot.
DT 21-FEB-2006, sequence version 3.
DT 07-MAR-2006, entry version 54.
DE Glutaredoxin-2, mitochondrial precursor (Thioltransferase)
DE (Glutathione-dependent oxidoreductase 2).
GN Name=GRX2; Synonyms=TRR, TTR1; OrderedLocusNames=YDR513W;
GN ORFNames=D9719.17;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=DMY6;
RX MEDLINE=92412147; PubMed=1530649;
RA Gan Z.-R.;
RT "Cloning and sequencing of a gene encoding yeast thioltransferase."
RL Biochem. Biophys. Res. Commun. 187:949-955(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288C;
RX MEDLINE=97313263; PubMed=9169867;
RA Jacq C., Alt-Moerbe J., Andre B., Arnold W., Bahr A., Ballesta J.P.G.,
Bargues M., Baron L., Becker A., Biteau N., Bloeker H., Blugeon C.,
Boskovic J., Brandt P., Bruckner M., Buitrago M.J., Coster F.,
Delaveau T., del Rey F., DuJon B., Eide L.G., Garcia-Cantalejo J.M.,
Goffeau A., Gomez-Peris A., Granotier C., Hanemann V., Hankeln T.,
Hohelsel J.D., Jaeger W., Jimenez A., Jonniaux J.-L., Kraemer C.,
Kuester H., Laamanen P., Legros Y., Louis E.J., Moeller-Rieker S.,
Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N.,
Paulin L., Perez J., Perez-Alonso M., Perez-Ortin J.E., Pohl T.M.,
Prydz H., Purnelle B., Rasmussen S.W., Renacha M.A., Revuelta J.L.,
Rieger M., Salom D., Saluz H.P., Saiz J.E., Saren A.-M., Schaefer M.,
Schaefer M., Schmidt E.R., Schneider C., Scholler P., Schwarz S.,
Soler-Mira A., Urrestazu L.A., Verhasselt P., Vissers S., Voet M.,
Volckaert G., Wagner G., Wambutt R., Wedler E., Wedler H., Woelfl S.,
Harris D.E., Bowman S., Brown D., Churcher C.M., Connor R., Dedman K.,
Gentles S., Hamlin N., Hunt S., Jones L., McDonald S., Murphy L.D.,
Niblett D., Odell C., Oliver K., Rajadream M.A., Richards C.,
Shore L., Walsh S.V., Barrell B.G., Dietrich F.S., Mulligan J.T.,
Allen E., Araujo R., Aviles E., Berno A., Carpenter J., Chen E.,
Cherry J.M., Chung E., Duncan M., Hunnicke-Smith S., Hyman R.W.,
Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K.,
Namath A., Oefner P., Oh C., Petel F.X., Roberts D., Schramm S.,
Schroeder M., Shogren T., Shroff N., Winant A., Yelton M.A.,
Botstein D., Davis R.W., Johnston M., Andrews S., Brinkman R.,
Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S.,
Greco T., Hallsworth K., Hawkins J., Millier L.W., Jier M.,
Johnson D., Johnston L., Kirsten J., Kucaba T., Langston Y.,
Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M.,

RA Pauley A., Peluso D., Rifkin L., Riles L., Taich A., Trevasakis E.,
 RA Vignati D., Wilcox L., Wohldman P., Vaudin M., Wilson R.,
 RA Waterston R., Albermann K., Hani J., Heumann K., Kleine K.,
 RA Mewes H.-W., Zollner A., Zaccaria P.;
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome IV.";
 RL Nature 387:75-78(1997).
 RN [3].
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RP STRAIN=S288c;
 RC Marischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,
 RA Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.,
 RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
 RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
 RA Lebar J.;
 RT "Creation of the YFLEX clone resource: cloning of *Saccharomyces cerevisiae* ORFs in the Gateway recombinational cloning system.";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RN [4].
 RP PROTEIN SEQUENCE OF 36-141.
 RX MEDLINE=90267489; PubMed=2189409;
 RA Gan Z.-R., Polokoff M.A., Jacobs J.W., Sardana M.K.;
 RT "Complete amino acid sequence of yeast thioltransferase (glutaredoxin).";
 RL Biochem. Biophys. Res. Commun. 168:944-951(1990).
 RN [5].
 RN FUNCTION, AND INDUCTION.
 RP PubMed=9571241;
 RX Luikenhuis S., Perrone G., Dawes I.W., Grant C.M.;
 RA "The yeast *Saccharomyces cerevisiae* contains two glutaredoxin genes that are required for protection against reactive oxygen species.";
 RT Mol. Biol. Cell 9:1081-1091(1998).
 RL [6].
 RN INDUCTION.
 RP PubMed=10786615;
 RX Grant C.M., Luikenhuis S., Beckhouse A., Soderbergh M., Dawes I.W.;
 RA "Differential regulation of glutaredoxin gene expression in response to stress conditions in the yeast *Saccharomyces cerevisiae*.";
 RT Biochim. Biophys. Acta 1490:33-42(2000).
 RL [7].
 RN SUBCELLULAR LOCATION.
 RP PubMed=11958675; DOI=10.1042/BJ20020570;
 RX Pedrajas J.R., Porras P., Martinez-Gallisteo E., Padilla C.A.,
 RA Miranda-Vizuet A., Barcena J.A.;
 RT "Two isoforms of *Saccharomyces cerevisiae* glutaredoxin 2 are expressed in vivo and localize to different subcellular compartments.";
 RL Biochem. J. 364:617-623(2002).
 RN [8].
 RN FUNCTION, AND BIOPHYSICO-CHEMICAL PROPERTIES.
 RX PubMed=11875065; DOI=10.1074/jbc.M11686200;
 RA Collinson E.J., Wheeler G.L., Garrido E.O., Avery S.V.,
 RA Grant C.M.;
 RT "The yeast glutaredoxins are active as glutathione peroxidases.";
 RL J. Biol. Chem. 277:16712-16717(2002).
 RN [9].
 RN FUNCTION, AND BIOPHYSICO-CHEMICAL PROPERTIES.
 RX PubMed=12684511; DOI=10.1074/jbc.M301387200;
 RA Collinson E.J., Grant C.M.;
 RT "Role of yeast glutaredoxins as glutathione S-transferases.";
 RL J. Biol. Chem. 278:22492-22497(2003).
 RN [10].
 RN LEVEL OF PROTEIN EXPRESSION.
 RX MEDLINE=22923965; PubMed=14562106; DOI=10.1038/nature02046;
 RA Ghaemmaghami S., Huh W.-K., Bower K., Howson R.W., Belle A.,
 RA Dephoure N., O'Shea E.K., Weissman J.S.;
 RT "Global analysis of protein expression in yeast.";
 RL Nature 425:737-741(2003).
 CC -!- FUNCTION: Multifunctional enzyme with glutathione-dependent oxidoreductase, glutathione peroxidase and glutathione S-transferase (GST) activity. The disulfide bond functions as an electron carrier in the glutathione-dependent synthesis of deoxyribonucleotides by the enzyme ribonucleotide reductase. In addition, it is also involved in reducing cytosolic protein- and nonprotein-disulfides in a coupled system with glutathione

CC reductase. Required for resistance to reactive oxygen species (ROS) by directly reducing hydroperoxides and for the detoxification of ROS-mediated damage.
 CC -!- BIOPHYSICO-CHEMICAL PROPERTIES:
 CC Kinetic parameters:
 CC KM=2.0 mM for H(2)O(2);
 CC KM=2.2 mM for tert-butyl hydroperoxide;
 CC KM=0.87 mM for cumene hydroperoxide;
 CC KM=0.17 mM for 1-chloro-2,4-dinitrobenzene;
 CC KM=0.27 mM for 1,2-dichloro-4-nitrobenzene;
 CC -!- SUBCELLULAR LOCATION: Cytoplasm, and mitochondrion. Two forms, a long and a short one are found in the mitochondrion, but only the short one is detected in the cytoplasm.
 CC -!- INDUCTION: In response to exposure to reactive oxygen species (ROS) and upon entry into stationary phase.
 CC -!- MISCELLANEOUS: Present with 31400 molecules/cell.
 CC -!- MISCELLANEOUS: It is unclear whether the long polypeptide observed in mitochondria represents the immature form of the protein before cleavage of the transit peptide and release of the short form into the cytoplasm or whether two mature isoforms exists.
 CC -!- SIMILARITY: Belongs to the glutaredoxin family.
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 CC -----
 CC EMBL: S45288; AAB23389.1; ALT_INIT; Genomic_DNA.
 DR EMBL: U33057; AAB64953.1; -; Genomic_DNA.
 DR EMBL: AY692896; AAT92915.1; -; Genomic_DNA.
 DR PIR: S69570; GDBY.
 DR HSSP: P44758; INM3.
 DR GeneOnline: 141005; -;
 DR Ensembl: YDR513JW; Saccharomycetes cerevisiae.
 DR SGD: S00002921; TTR1.
 DR LinkHub: P17695; -;
 DR GO: GO:0005829; C:cytosol; IDA.
 DR GO: GO:0005739; C:mitochondrion; IDA.
 DR GO: GO:0004602; F:glutathione peroxidase activity; IDA.
 DR GO: GO:0004364; F:glutathione transferase activity; IDA.
 DR GO: GO:0030508; F:thiol-disulfide exchange intermediate activity; IMP.
 DR GO: GO:0030503; P:regulation of cell redox homeostasis; IDA.
 DR GO: GO:0006979; P:response to oxidative stress; IMP.
 DR PROSITE: PS00195; GLUTAREDOXIN; 1.
 KW Complete proteome; Direct protein sequencing; Electron transport;
 KW Mitochondrion; Redox-active center; Transit peptide; Transport.
 FT TRANSIT 1 35 Mitochondrion.
 FT CHAIN 36 143 Glutaredoxin-2.
 FT /FTID=PRO 0000141612.
 FT DISULFID 61 64 Redox-active.
 FT SEQUENCE 143 AA; 15861 MW; 99A79B87695B2266 CRC64;
 Query Match 100.0%; Score 714; DB 1; Length 143;
 Best Local Similarity 100.0%; Pred. No. 3.1e-55;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METNRFSDNLVILIIITLFIATRIIAKRLSPKVMVQSTVAHVKDLIGQKEVFVAAKTY 60
 DB 1 METNRFSDNLVILIIITLFIATRIIAKRLSPKVMVQSTVAHVKDLIGQKEVFVAAKTY 60
 QY 61 CPYCKATSLTLFQELNVPKSKALVLELDEMSNGSEIQDALEISGQKTVPNVYINGKHIG 120
 DB 61 CPYCKATSLTLFQELNVPKSKALVLELDEMSNGSEIQDALEISGQKTVPNVYINGKHIG 120
 QY 121 GNSDLETLKKGKLAELIKPVFQ 143
 DB 121 GNSDLETLKKGKLAELIKPVFQ 143
 RESULT 2
 GLRX1 YEAST
 ID GLRX1 YEAST STANDARD; PRT; 110 AA.
 AC P25373;
 DT 01-MAY-1992, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAY-1992, sequence version 1.

[illegible]

61 DIQAALYEINGQRTVPNIYNGKHGGNDLQELRTGETLELELEPI 107

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Db
RESULT 3
Q6CUI6 KLULA
ID Q6CUI6 KLULA PRELIMINARY; PRT; 107 AA.
AC Q6CUI6
OC Q6CUI6
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DE 07-FEB-2006, entry version 17.
DE Similar to sp|P25373|Saccharomyces cerevisiae YCL035c GRX1
DE Glutaredoxin.
DE OrderedLocNames=KLA0C01298g;
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrast A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.-M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O.,
RA Pallenz S., Potier S., Richard G.-P., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Jouvel M., Weschof E., Wirth B.,
RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouclier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
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EMBL: CR382123; CAH01104.1; -; Genomic DNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0045454; P:cell redox homeostasis; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR011767; GLR_AS.
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR011899; GRX_euk.
DR InterPro; IPR012336; Thioridoxin-like fd.
DR Pfam; PF00462; Glutaredoxin; 2.
DR PRINTS; PR00160; GLUTAREDOXIN.
DR TIGRPFAMs; TIGR02180; GRX_euk; 1.
DR PROSITE; PS00195; GLUTAREDOXIN; UNKNOWN 1.
KW Complete proteome; Electron transport; Redox-active center; Transport.
SQ SEQUENCE 107 AA; 11565 MW; 7ECB0E9006505DA5 CRC64;
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Query Match 46.6%; Score 333; DB 2; Length 107;
Best Local Similarity 59.6%; Pred. No. 1.4e-21;
Matches 62; Conservative 20; Mismatches 22; Indels 0; Gaps 0;
QY 35 MVQSETVAHVKDLIGQKEVFAAKTYPYCKATLSTLTFQELNVPKSKALVLEDSNGS 94
Db 1 MPSAATIAVQGLINSKIEFVASKTYPYQATLTKLTFEEKVKDKKLTATVQLNQLDGS 60
QY 95 EIDDALEIEISGQTPVNPVINGKHGGNSDLETKKNGKLAETIL 138
Db 61 DIQDAALAEITGQKTPNIFNGKHGGNSDLETKKNGKLAETIL 104
RESULT 4
Q751W5 ASHGO
ID Q751W5 ASHGO PRELIMINARY; PRT; 111 AA.
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AC Q751W5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE AFR710WP.
GN OrderedLocNames=AFR710W;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
RA Gaffney T.D., Philippsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
RT Saccharomyces cerevisiae genome.";
RL Science 304:304-307(2004).
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EMBL: A3016819; AAS54082.1; -; Genomic DNA.
DR HSSP; P35754; 1B4Q.
DR AGD; AFR710W; -.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0045454; P:cell redox homeostasis; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR011767; GLR_AS.
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR011899; GRX_euk.
DR InterPro; IPR012336; Thioridoxin-like fd.
DR InterPro; IPR012335; Thioridoxin_fold.
DR Pfam; PF00462; Glutaredoxin; 2.
DR PRINTS; PR00160; GLUTAREDOXIN.
DR TIGRPFAMs; TIGR02180; GRX_euk; 1.
DR PROSITE; PS00195; GLUTAREDOXIN; UNKNOWN 1.
KW Complete proteome; Electron transport; Redox-active center; Transport.
SQ SEQUENCE 111 AA; 12152 MW; 98F44CD1BC1536F0 CRC64;
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Query Match 42.9%; Score 306.5; DB 2; Length 111;
Best Local Similarity 55.7%; Pred. No. 3.3e-19;
Matches 59; Conservative 19; Mismatches 27; Indels 1; Gaps 1;
QY 35 MVQSETVAHVKDLIGQKEVFAAKTYPYCKATLSTLTFQELNVPKSKALVLEDEM-SNG 93
Db 1 MVSPSVIKQVQALIQNRRVFIASKTYPYQAAKRTLLEKRVPAVAKLLEDTWGEG 60
QY 94 SEIQDALEIEISGQTPVNPVINGKHGGNSDLETKKNGKLAETILK 139
Db 61 AVTQAALQELSGQRTVPNIYNGKHGGNSDLETKKNGKLAETIL 106
RESULT 5
QSABBI CANAL
ID QSABBI CANAL PRELIMINARY; PRT; 119 AA.
AC QSABBI;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Potential mitochondrial glutaredoxin.
GN Names=Trt11; ORFNames=CaO19.13480, CaO19.6059;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
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RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RA "The diploid genome sequence of Candida albicans.";
RA Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; AACQ01000036; EAL00015.1; -; Genomic DNA.
DR EMBL; AACQ01000035; EAL00120.1; -; Genomic DNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0045454; P:cell redox homeostasis; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR011767; GLR AS.
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR011899; GRX euk.
DR InterPro; IPR012336; Thioridoxin-like fd.
DR InterPro; IPR012335; Thioridoxin_fold.
DR Pfam; PF00462; Glutaredoxin; 2.
DR PRINTS; PR00160; GLUTAREDOXIN.
DR TIGRFAMs; TIGR02180; GRX euk; 1.
DR PROSITE; PS00195; GLUTAREDOXIN; UNKNOWN 1.
DR KW Electron transport; Redox-active center; Transport.
DR KW Electron transport; Redox-active center; Transport.
SQ SEQUENCE 119 AA; 13124 MW; 3EB431493A46565C CRC64;

Query Match 42.1%; Score 300.5; DB 2; Length 119;
Best Local Similarity 50.4%; Pred. No. 1.2e-18;
Matches 61; Conservative 24; Mismatches 31; Indels 5; Gaps 2;

QY 19 LEATRIIAKPLSPKMKVSOETVAHVKDLIGQKVFVAAKTYCPYCKATLSTLFLQELNVP 78
DB 1 MFT-LTKLFNTSTWSSQVKNKVEQLIKTRPVFIASKSCPYCATKST-----IEAI 55

QY 79 KSKALVLELDEMNGSBIQDALEISGQKTPVNVYINGKHIGNSDLETLLKNGKLAEL 138
DB 56 TKDAYILLEVDVGGIQAIEALLEITQRTVPNVFIQGGHIGNSDVQALKSSDKLDKI 115

QY 139 K 139
DB 116 K 116

RESULT 6
Q6BIM4_DEBHA
ID Q6BIM4_DEBHA PRELIMINARY; PRT; 104 AA.
AC Q6BIM4;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DE Similar to CA4919|CATTR1 Candida albicans CATTR1 Glutaredoxin.
GN OrderedLocNames=DEHAOG09966g;
OS Debaryomyces hansenii (Yeast) (Torulasporea hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=4959;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 36239 / CBS 767;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykascen C.,
RA Boissrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Nicoud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zénou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
CC Nature 430:35-44(2004).
CC -----
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RA Zénou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
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CC -----
CC EMBL; CR382139; CAG90415.1; -; Genomic DNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0045454; P:cell redox homeostasis; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR011767; GLR AS.
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR011899; GRX euk.
DR InterPro; IPR012336; Thioridoxin-like fd.
DR InterPro; IPR012335; Thioridoxin_fold.
DR Pfam; PF00462; Glutaredoxin; 2.
DR TIGRFAMs; TIGR02180; GRX euk; 1.
DR PROSITE; PS00195; GLUTAREDOXIN; UNKNOWN 1.
DR KW Complete proteome; Electron transport; Redox-active center; Transport.
DR KW Complete proteome; Electron transport; Redox-active center; Transport.
SQ SEQUENCE 104 AA; 11393 MW; 1515F4DE0EAAAB96 CRC84;

Query Match 38.7%; Score 276; DB 2; Length 104;
Best Local Similarity 52.3%; Pred. No. 1.6e-16;
Matches 56; Conservative 20; Mismatches 27; Indels 4; Gaps 2;

QY 35 MVSQETVAHVKDLIGQKVFVAAKTYCPYCKATLSTLFLQELNVPKSKALVLEDEMNGS 94
DB 1 MVSQETTDKVVQQLIKTRPVFIASKSCPYCATKNTI---SSITKO-AYIILEDVEDGS 56

QY 95 EIQDALEETSGQKTPVNVYINGKHIGNSDLETLLKNGKLAELTKPV 141
DB 57 EIQDALEYLTGQKTPVNVFIQGGHIGNSDVQELSGDKLESKIKAV 103

RESULT 7
Q6CCY8_YARLI
ID Q6CCY8_YARLI PRELIMINARY; PRT; 105 AA.
AC Q6CCY8;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Similar to sp|P17695|Saccharomyces cerevisiae Glutaredoxin.
GN OrderedLocNames=YALI0C05467g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=CLIB 122 / E 150;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykascen C.,
RA Boissrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zénou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
CC Nature 430:35-44(2004).
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CC -----
DR EMBL; CR382129; CAG81775.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0045454; P:cell redox homeostasis; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR011767; GLR_AS.
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR011899; GRX euk.
DR InterPro; IPR012336; Thioredoxin-like fd.
DR InterPro; IPR006663; Thioredox dom2.
DR InterPro; IPR012335; Thioredoxin_fold.
DR Pfam; PF00462; Glutaredoxin; 2.
DR PRINTS; PR00160; GLUTAREDOXIN.
DR TIGRFAMs; TIGR02180; GRX euk; 1.
DR PROSITE; PS00195; GLUTAREDOXIN; 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
DR Complete proteome.
KW Redox-active center; Transport.
SQ SEQUENCE 105 AA; 11427 MW; 95492161A6F90024 CRC64;

Query Match 38.0%; Score 271.5; DB 2; Length 105;
Best Local Similarity 48.6%; Pred. No. 4e-16;
Matches 51; Conservative 26; Mismatches 25; Indels 3; Gaps 1;

QY 35 MVSOETVAHVKDLIGQEVFAAKTCYPCYCKATLSTLFOELNVPKSKALVLELDEMSNGS 94
DB 1 MATESAIKTIKEHAKDKVFAVSKSCYPCYCKQTKQLSQ---FKEAKPVILELDELDDGA 57

QY 95 EIQDALEIEISGQKTPVNVYINGKHGIGNSDLTKLXNGKLAELIK 139
DB 58 ELQAALAEITGQRTVNVFVIGGHHGIGNSDLQVLAQKDELADKIK 102

RESULT 8
Q4IL11 GIBZE
ID Q4IL11 GIBZE PRELIMINARY; PRT; 106 AA.
AC Q4IL11.
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 18-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein.
GN ORFNames=FG02097.1.
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC SPRAIN-PH-1 / NRRL 31084.
RA Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Archachl H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D.,
RA Galagan J.E., Gardyna S., Gnerre S., Graham M., Grand-Pierre N.,
RA Hafez N., Hagoopian D., Hagos B., Hall J., Horton L., Hulme W.,
RA Iliev I., Jaffe D., Johnson R., Jones C., Kamal M., Kanat A.,
RA Karakas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
RA Lui A., Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J.,
RA Manning J., Mathews C., Mauceli E., McCarthy M., Meldrim J.,
RA Menues L., Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C.,
RA Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
RA O'Neill D., Oliver J., Peterson K., Phunkhang P., Pierre N.,
RA Purcell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C.,
RA Rogov P., Roman J., Schauer S., Schuback R., Seaman S., Severy P.,
RA Spirnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N.,
RA Stubbs M., Talamas J., Teafaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.S.;
RC "Fusarium graminearum genome sequence.";
RT Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RL
CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AACM01000111; EAA69728.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0045454; P:cell redox homeostasis; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR011767; GLR_AS.
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR011899; GRX euk.
DR InterPro; IPR012336; Thioredoxin-like fd.
DR InterPro; IPR006662; Thioredo.
DR InterPro; IPR006663; Thioredox dom2.
DR Pfam; PF00462; Glutaredoxin; 1.
DR PRINTS; PR00160; GLUTAREDOXIN.
DR TIGRFAMs; TIGR02180; GRX euk; 1.
DR PROSITE; PS00195; GLUTAREDOXIN; 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
DR Complete proteome; Electron transport; Hypothetical protein;
KW Redox-active center; Transport.
SQ SEQUENCE 106 AA; 11646 MW; 162C3522D6205893 CRC64;

Query Match 36.8%; Score 263; DB 2; Length 106;
Best Local Similarity 56.2%; Pred. No. 2.3e-15;
Matches 54; Conservative 17; Mismatches 21; Indels 4; Gaps 2;

QY 44 VKDLIGQKEVFAAKTCYPCYCKATLSTLFOELNVPKSKALVLELDEMSNGSRIQDALEEI 103
DB 8 VQQLIDNNSVVVFSKSCYPCYCKQTKTL--DDLN---TEYELLELDEVAQGSALQDALEKI 63

QY 104 SQGKTPVNVYINGKHGIGNSDLTKLXNGKLAELIK 139
DB 64 SGQRTVNVYIKQHHGIGNSDLQSLNSGKLNLLK 99

RESULT 9
Q3MPD5 CANAL
ID Q3MPD5 CANAL PRELIMINARY; PRT; 156 AA.
AC Q3MPD5.
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein Cad7.0240.
GN Name=Cad7.0240; ORFNames=CaO19.6509;
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=15937140; DOI=10.1534/genetics.104.034652;
RA Chibana H., Oka N., Nakayama H., Aoyama T., Magee B.B., Magee P.T.,
RA Mikami Y.;
RT "Sequence finishing and gene mapping for Candida albicans chromosome 7
RT and syntenic analysis against the Saccharomyces cerevisiae genome.";
RL Genetics 170:1525-1537(2005).
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CC -----
DR EMBL; AF006852; BAE44725.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0045454; P:cell redox homeostasis; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR011767; GLR_AS.
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR011899; GRX euk.
DR InterPro; IPR012336; Thioredoxin-like fd.
DR InterPro; IPR006662; Thioredo.
DR Pfam; PF00462; Glutaredoxin; 1.
```

DR PRINTS; PR00160; GLUTAREDOXIN.
 DR TIGRFAMS; TIGR02180; GRX euk; 1.
 DR PROSITE; PS00195; GLUTAREDOXIN; 1.
 DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN 1.
 KW Electron transport; Hypothetical protein; Redox-active center;
 KW Transport.
 SQ SEQUENCE 156 AA; 17779 MW; 6BA47C9B9702F6D8 CRC64;

Query Match 35.5%; Score 253.5; DB 2; Length 156;
 Best Local Similarity 40.3%; Pred. No. 2.4e-14;
 Matches 56; Conservative 28; Mismatches 40; Indels 15; Gaps 5;

QY 4 NFSFSDNLVILIIITLPAIRIAKRLFLSTPKMVSQETVAHVHKLIGQKEVFAAKTYCPY 63
 DB 32 SLSYQPNFVMSLIGW-----LSSWFQNEP--ITPELKKEIESNINSHKVLVYSKSYCPY 84
 QY 64 CKATLSTLFOELNVKSKALVLEDEMSNGSEITQDALEEISGQKTPNVVINGKHIGNS 123
 DB 85 CTST-KTLQSLN---QDYKVIELDQIPKGSALQNGLOELTGQRTVPNVFINGKHIGNS 140
 QY 124 DLETLKNGKLAELKPVF 142
 DB 141 DIQALHSQK-----LKPLF 155

RESULT 10
 Q5AH29 CANAL PRELIMINARY; PRT; 156 AA.
 AC Q5AH29;
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 26-APR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Potential glutaredoxin.
 GN Name=TR12; ORFNames=CaO19.13862, CaO19.6509;
 OS Candida albicans SC5314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=237561;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SC5314;
 RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
 RA Jones T., Federpiel N.A., Chibana H., Dungan J., Kalman S.,
 RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
 RA Davis R.W., Scherer S.;
 RT "The diploid genome sequence of Candida albicans";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC -----
 CC EMBL; AACQ0100020; EAL02011.1; -; Genomic DNA.
 DR EMBL; AACQ0100016; EAL02545.1; -; Genomic DNA.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0045454; P:cell redox homeostasis; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR002109; Glutaredoxin.
 DR InterPro; IPR011767; GLR AS.
 DR InterPro; IPR011899; GRX euk.
 DR InterPro; IPR012336; Thiorxn-like_fd.
 DR InterPro; IPR006662; Thiorxn.
 DR Pfam; PF00462; Thiorxn_fold.
 DR PRINTS; PR00160; GLUTAREDOXIN; 2.
 DR TIGRFAMS; TIGR02180; GRX euk; 1.
 DR PROSITE; PS00195; GLUTAREDOXIN; UNKNOWN 1.
 DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN 1.
 KW Electron transport; Redox-active center; Transport.
 SQ SEQUENCE 156 AA; 17779 MW; 6BA47C9B9702F6D8 CRC64;

Query Match 35.5%; Score 253.5; DB 2; Length 156;
 Best Local Similarity 40.3%; Pred. No. 2.4e-14;
 Matches 56; Conservative 28; Mismatches 40; Indels 15; Gaps 5;

QY 4 NFSFSDNLVILIIITLPAIRIAKRLFLSTPKMVSQETVAHVHKLIGQKEVFAAKTYCPY 63
 DB 32 SLSYQPNFVMSLIGW-----LSSWFQNEP--ITPELKKEIESNINSHKVLVYSKSYCPY 84
 QY 64 CKATLSTLFOELNVKSKALVLEDEMSNGSEITQDALEEISGQKTPNVVINGKHIGNS 123
 DB 85 CTST-KTLQSLN---QDYKVIELDQIPKGSALQNGLOELTGQRTVPNVFINGKHIGNS 140
 QY 124 DLETLKNGKLAELKPVF 142
 DB 141 DIQALHSQK-----LKPLF 155

RESULT 11
 Q5B5G5 EMENI PRELIMINARY; PRT; 102 AA.
 AC Q5B5G5;
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 26-APR-2005, sequence version 1.
 DT 07-MAR-2006, entry version 11.
 DE Hypothetical protein.
 GN ORFNames=AN4215.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=FGSC 4;
 RX PubMed=16372000; DOI=10.1038/nature04341;
 RA Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,
 RA Batzoglou S., Lee S.-I., Bastuerkmen M., Spevak C.C., Clutterbuck J.,
 RA Kapitonov V., Jurka J., Sczarcchio C., Farman M., Butler J.,
 RA Purcell S., Harris S., Braus G.H., Draht O., Busch S., D'Enfert C.,
 RA Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,
 RA Doonan J.H., Yu J., Vlenken K., Pain A., Freitag M., Selker E.U.,
 RA Archer D.B., Penalva M.A., Oakley B.R., Momany M., Fanaka T.,
 RA Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W.,
 RA Caddick M., Hynes M., Paoletti M., Fischer R., Miller B.L., Dyer P.S.,
 RA Sachs M.S., Osmani S.A., Birren B.W.;
 RT "Sequencing of Aspergillus nidulans and comparative analysis with A.
 RT fumigatus and A. oryzae";
 RL Nature 438:1103-1115 (2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC -----
 CC EMBL; AACD0100068; EAA59314.1; -; Genomic DNA.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0045454; P:cell redox homeostasis; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR002109; Glutaredoxin.
 DR InterPro; IPR011899; GRX euk.
 DR InterPro; IPR012336; Thiorxn-like_fd.
 DR InterPro; IPR006662; Thiorxn.
 DR InterPro; IPR006663; Thiorxn_dom2.
 DR Pfam; PF00462; Thiorxn_fold.
 DR PRINTS; PR00160; GLUTAREDOXIN; 1.
 DR TIGRFAMS; TIGR02180; GRX euk; 1.
 DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN 1.
 KW Hypothetical protein; Redox-active center.
 SQ SEQUENCE 102 AA; 10960 MW; 91398F30245E16E3 CRC64;

Query Match 33.4%; Score 238.5; DB 2; Length 102;
 Best Local Similarity 48.2%; Pred. No. 3.3e-13;


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Matches 53; Conservative 23; Mismatches 21; Indels 13; Gaps 4;

Qy 30 LSTPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFQELNVPKSKALVLELDE 89
Db 1 MSSAKVKAQQ-----IIDENGWVVFSSKSPYCKASKS--LLSELG---AKTYALELDT 49
Qy 90 MNSGSEIQDALEEISGQKTPVNVYINGKHIGNSDLETLKNGKLAELIK 139
Db 50 IDGADLQDALEEISGQKTPVNVYIYAKKHIGNSDLQGIKKO--LPALLK 97

RESULT 12
O6BT54.DEBHA
ID Q6BT54.DEBHA PRELIMINARY; PRT; 113 AA.
AC Q6BT54;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Similar to ca|CA4964|IPF3920 Candida albicans IPF3920.
GN OrderedLocusNames=DEHA0D041369;
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=4959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 36219 / CBS 767;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolaki M., Ostas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).

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CC -----
DR EMBL, CR382136; CAG86752.1; -; Genomic_DNA.
DR GO, GO:0005489; F:electron transporter activity; IEA.
DR GO, GO:0045454; P:cell redox homeostasis; IEA.
DR GO, GO:0006118; P:electron transport; IEA.
DR InterPro, IPRO11767; GLR AS.
DR InterPro, IPRO2109; Glutaredoxin.
DR InterPro, IPRO11895; GRX euk.
DR InterPro, IPRO12336; Thioridoxin-like fd.
DR InterPro, IPRO06663; Thioridoxin_dom2.
DR InterPro, IPRO12335; Thioridoxin_fold.
DR Pfam, PF00462; Glutaredoxin; 2.
DR PRINTS, PR00160; GLUTAREDOXIN.
DR TIGRfams, TIGR02180; GRX_euk; 1.
DR PROSITE, PS00195; GLUTAREDOXIN; 1.
KW Complete proteome.
SQ SEQUENCE 113 AA; 12578 MW; 65A968395156E096 CRC64;

Query Match 32.5%; Score 232; DB 2; Length 113;
Best Local Similarity 45.5%; Pred. No. 1.4e-12;
Matches 50; Conservative 21; Mismatches 33; Indels 6; Gaps 3;

Qy 29 FLSTPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFQELNVPKSKALVLELDE 88
Db 9 FVSPPP--VSPVKAQVQLNLSNKLIFLKSYPYCDST-KDLIKSIT---SDPKVVELN 62

Matches 53; Conservative 23; Mismatches 21; Indels 13; Gaps 4;

Qy 89 EMSNGSEIQDALEEISGQKTPVNVYINGKHIGNSDLETLKNGKLAELIK 138
Db 63 TSANGRTIQDALEEMTGQNTVPNIFINRKHIGNSDLQALQAGAKLSLV 112

RESULT 13
Q2UU38.ASPOR
ID Q2UU38.ASPOR PRELIMINARY; PRT; 102 AA.
AC Q2UU38;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE Predicted protein.
DE Predicted protein.
GN ORFNames=AQ090009000473;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RIB 40;
RX PubMed=16372010; DOI=10.1038/nature04300;
RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Goni K.,
RA Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,
RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,
RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Maeda H., Maeyama N.,
RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,
RA Kuhara S., Ogasawara N., Kikuchi H.;
RT "Genome sequencing and analysis of Aspergillus oryzae.";
RL Nature 438:1157-1161 (2005).

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CC -----
DR EMBL, AP007150; BAE54927.1; -; Genomic_DNA.
KW Redox-active center.
SQ SEQUENCE 102 AA; 10925 MW; 3FOA6FB970952CD CRC64;

Query Match 32.3%; Score 230.5; DB 2; Length 102;
Best Local Similarity 48.2%; Pred. No. 1.7e-12;
Matches 53; Conservative 17; Mismatches 27; Indels 13; Gaps 3;

Qy 30 LSTPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFQELNVPKSKALVLELDE 89
Db 1 MSAAKIKAQ-----GIINANAVVFSKSPYCKSKSLSQ-----LDKYLTIELDE 49
Qy 90 MNSGSEIQDALEEISGQKTPVNVYINGKHIGNSDLETLKNGKLAELIK 139
Db 50 ESDGSAIQDALEIVEISGQRTVPNIFIKQKHIGNSDLQARK--SELPALLK 97

RESULT 14
Q9P718.NEUCR
ID Q9P718.NEUCR PRELIMINARY; PRT; 109 AA.
AC Q9P718;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-MAR-2006, entry version 19.
DE Probable glutaredoxin.
GN Name=8D4.220;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
```



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RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN (2)  
RP NUCLEOTIDE SEQUENCE.  
RA German Neurepoira genome project;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
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CC -----  
CC EMBL: ALJ35819; CAB88564.1; -, Genomic_DNA.  
DR PIR: T48748; T48748.  
DR HSP: P12309; LKTE.  
DR GO: GO:0005489; F:electron transporter activity; IEA.  
DR GO: GO:0045454; P:cell redox homeostasis; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR InterPro: IPR002110; ANK.  
DR InterPro: IPR011767; GUR_AS.  
DR InterPro: IPR002109; Glutaredoxin.  
DR InterPro: IPR011899; GRX_euk.  
DR InterPro: IPR012336; ThiOrdxn-like_fd.  
DR InterPro: IPR006662; ThioRed.  
DR InterPro: IPR006663; ThioRedox dom2.  
DR Pfam: PF00462; ThioRedoxin_fold.  
DR PRINTS: PR0012335; ThioRedoxin_1.  
DR PRINTS: PR01415; ANKYRIN.  
DR TIGRFAMs: TIGR02180; GRX_euk; 1.  
DR PROSITE: PS00195; GLUTAREDOXIN; 1.  
DR PROSITE: PS00194; THIOREDOXIN; UNKNOWN_1.  
DR Electron transport; Redox-active center; Transport.  
KW SEQUENCE 109 AA; 11788 MW; 7E262272E84A1BE1 CRC64;  
SQ  
Query Match 31.4%; Score 224; DB 2; Length 109;  
Best Local Similarity 42.6%; Pred. No. 6.8e-12;  
Matches 46; Conservative 22; Mismatches 36; Indels 4; Gaps 1;  
QY 36 VSQETVAHVQDLIGQKEVFVAAKTYCPYCKATSTLFLQELNVPKSKALVLELDMSGSE 95  
DB 1 MSDAATQKAKQLINDNAVVFYSKYPYCSNTK----QILDGLNAKYATVELNQESDGS 56  
QY 96 IQDALEEISGQKTVNPKYNGKHIGNSDLETLLKNGKGLAEILKVPFQ 143  
DB 57 VQDALLKLTGQRTVPNIFIGKHIGNSDLEAVVNGKNGKGIQELIQ 104  
RESULT 15  
Q8S3L1_9ROSI  
ID Q8S3L1_9ROSI PRELIMINARY; PRT; 139 AA.  
AC Q8S3L1;  
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2002, sequence version 1.  
DT 21-FEB-2006, entry version 19.  
DE Glutaredoxin.  
OS Populus tremula x Populus tremuloides.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.  
OX NCBI_TaxID=47664;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21848454; PubMed=11858718; DOI=10.1006/prep.2001.1574;  
RA Rouhier N., Gelhaye E., Sautiere P.E., Jacquot J.P.;  
RT "Enhancement of poplar glutaredoxin expression by optimization of the  
RT cDNA sequence."  
RL Protein Expr. Purif. 24:234-241(2002).  
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CC -----  
CC EMBL: AF483267; AAL90750.1; -, mRNA.  
DR HSP: P44758; 1NN3.  
DR GO: GO:0005489; F:electron transporter activity; IEA.
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DR GO: GO:0045454; P:cell redox homeostasis; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR InterPro: IPR011767; GUR_AS.  
DR InterPro: IPR002109; Glutaredoxin.  
DR InterPro: IPR011899; GRX_euk.  
DR InterPro: IPR012336; ThiOrdxn-like_fd.  
DR InterPro: IPR006662; ThioRed.  
DR InterPro: IPR006663; ThioRedox dom2.  
DR Pfam: PF00462; ThioRedoxin_fold.  
DR PRINTS: PR0012335; ThioRedoxin_1.  
DR PRINTS: PR01415; ANKYRIN.  
DR TIGRFAMs: TIGR02180; GRX_euk; 1.  
DR PROSITE: PS00195; GLUTAREDOXIN; UNKNOWN_1.  
DR PROSITE: PS00194; THIOREDOXIN; UNKNOWN_1.  
DR Electron transport; Redox-active center; Transport.  
KW SEQUENCE 139 AA; 15192 MW; C3527C3F1F54CB2D CRC64;  
SQ  
Query Match 30.4%; Score 217; DB 2; Length 139;  
Best Local Similarity 35.5%; Pred. No. 3.7e-11;  
Matches 49; Conservative 25; Mismatches 52; Indels 12; Gaps 3;  
QY 1 METNFSFDSNLIVIIITLTPATRIIAKRFILSTPMVVSQETVAHVQDLIGQKEVFVAAKTY 60  
DB 1 MATRIRLPSILATAVTLTVLAA-----SLTWAAGSPEATFVKKTISHQIVIFSKEY 52  
QY 61 CPYCKATLSTLFOELNVPKSKALVLELDMSGSEIQTDALEEISGQKTVNPKYNGKHIG 120  
DB 53 CPYCKKA-KGVFKELN---QTPHVVELDQREDGHDIDAMSEIVGRRTVPQVFDGKHIG 108  
QY 121 GNSDLETLLKNGKGLAEIL 138  
DB 109 GSDDTVEAYESGELAKLL 126  
Search completed: November 6, 2006, 19:17:08  
Job time : 305 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2006, 19:17:25 ; Search time 53 Seconds
(without alignments)
236.168 Million cell updates/sec

Title: US-10-523-362-4

Perfect score: 714

Sequence: 1 METNFSFSDNLVILIIITLF.....DLETLKNGKLAEILKPVFQ 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /EMC Celerra SID33/ptodata/2/iaa/5 COMB.pcp.*
- 2: /EMC Celerra SID33/ptodata/2/iaa/6 COMB.pcp.*
- 3: /EMC Celerra SID33/ptodata/2/iaa/7 COMB.pcp.*
- 4: /EMC Celerra SID33/ptodata/2/iaa/H COMB.pcp.*
- 5: /EMC Celerra SID33/ptodata/2/iaa/RECTUS COMB.pcp.*
- 6: /EMC Celerra SID33/ptodata/2/iaa/RE COMB.pcp.*
- 7: /EMC Celerra SID33/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257.5	36.1	193	2	US-09-248-796A-18115
2	200	28.0	102	1	US-08-911-319A-4
3	200	28.0	102	2	US-09-352-619-4
4	196.5	27.5	137	2	US-09-270-767-32387
5	196.5	27.5	137	2	US-09-270-767-47604
6	174	24.4	60	2	US-09-248-796A-18114
7	173	24.2	114	2	US-09-621-976-5130
8	173	24.2	164	1	US-08-911-319A-1
9	173	24.2	164	2	US-09-352-619-1
10	151.5	21.2	106	2	US-09-162-564-3
11	146	20.4	94	2	US-09-621-976-5132
12	145	20.3	105	2	US-09-162-564-5
13	144.5	20.2	107	2	US-09-162-564-6
14	144	20.2	106	2	US-09-162-564-2
15	143	20.0	106	1	US-08-911-319A-3
16	143	20.0	106	2	US-09-352-619-3
17	143	20.0	106	2	US-09-162-564-4
18	143	20.0	106	2	US-09-513-999C-8053
19	142.5	20.0	105	2	US-09-538-092-1085
20	136	19.0	95	1	US-08-911-319A-5
21	136	19.0	95	2	US-09-352-619-5
22	129	18.1	115	2	US-09-902-540-10580
23	126.5	17.7	196	2	US-09-248-796A-18117
24	109.5	15.3	51	2	US-09-621-976-5131
25	108	15.1	95	2	US-09-328-352-8011
26	104.5	14.6	109	2	US-09-540-236-2497

ALIGNMENTS

RESULT 1

US-09-248-796A-18115
; Sequence 18115, Application US/09248796A
; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 18115

; LENGTH: 193

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-18115

Query Match 36.1%; Score 257.5; DB 2; Length 193;

Best Local Similarity 40.3%; Pred. No. 1.4e-22;

Matches 56; Conservative 29; Mismatches 39; Indels 15; Gaps 5;

Qy 4 NFEFSDNLVILIIITLFATRIIAKRLSTPKMVSQETVAHVKDILGQKEVFVAAKTYCPY 63

Db 69 SLSYQNFVMSLLIGW-----LSSWFQNEP--ITPELKEIESNINSHKVLVYSKVCYPY 121

Qy 64 CKATLSTLFLQELNVPKSKALVLEDEMSNGSEIQDALEEISGQKTVPNVYINGKHGNS 123

Db 122 CTST-NTLLQSLN--QDVKVIEDQIPKGSALQNGELTQGTVPNVFINGKHGNS 177

Qy 124 DLETLKNGKLAEILKPVF 142

Db 178 DIQALHSQKQ---LKLPLF 192

RESULT 2

US-08-911-319A-4

; Sequence 4, Application US/08911319A

; Patent No. 5968798

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Corley, Neil C.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA

; NUMBER OF SEQUENCES: 6

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,319A
; FILING DATE: August 14, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Muenzen, Colette C.
; REGISTRATION NUMBER: 39,784
; REFERENCE/DOCKET NUMBER: PF-0363 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1732424
; US-08-911-319A-4

Query Match 28.0%; Score 200; DB 1; Length 102;
Best Local Similarity 46.8%; Pred. No. 4.3e-16;
Matches 44; Conservative 14; Mismatches 32; Indels 4; Gaps 2;

QY 45 KDLIGQKEVFVAATYCPYCKATLSTLFQELNVPKSKALVLELDENSGNSEIQDAAEEIS 104
Db 7 KELVCSNAVVFSTKYPCYC-TSVKKLLDQLG---AKYKVELDTSDESGSEIQTALAWEI 62

QY 105 GQKTPNVYINGKHGNSDLETLKXNGKLAEL 138
Db 63 GQRTVPNVFVGKHGGCDSTTAKHSQGQLVPLL 96

US-08-911-319A-4

RESULT 3
US-09-352-619-4
; Sequence 4, Application US/09352619
; Patent No. 6084070
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/352,619

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PF-0363 US
; REGISTRATION NUMBER: 39,784
; REFERENCE/DOCKET NUMBER: PF-0363 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1732424
; US-09-352-619-4

Query Match 28.0%; Score 200; DB 2; Length 102;
Best Local Similarity 46.8%; Pred. No. 4.3e-16;
Matches 44; Conservative 14; Mismatches 32; Indels 4; Gaps 2;

QY 45 KDLIGQKEVFVAATYCPYCKATLSTLFQELNVPKSKALVLELDENSGNSEIQDAAEEIS 104
Db 7 KELVCSNAVVFSTKYPCYC-TSVKKLLDQLG---AKYKVELDTSDESGSEIQTALAWEI 62

QY 105 GQKTPNVYINGKHGNSDLETLKXNGKLAEL 138
Db 63 GQRTVPNVFVGKHGGCDSTTAKHSQGQLVPLL 96

US-09-352-619-4

RESULT 4
US-09-270-767-32387
; Sequence 32387, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32387
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-32387

Query Match 27.5%; Score 196.5; DB 2; Length 137;
Best Local Similarity 37.6%; Pred. No. 1.8e-15;
Matches 44; Conservative 26; Mismatches 36; Indels 11; Gaps 4;

QY 30 LSTPKMVSQETVAH---VKDLIGQKEVFVAATYCPYCKATLSTLFQELNVPKSKALVLE 86
Db 25 LQRTLYVMSDSSHAQFVRDTISGNKVVIFSKYCDPYC-SMAKEQPKINV---KATVIE 80

QY 87 LDEMSNGSEIQDAAEEISGQKTPNVYINGKHGNSDLETLKXNGKLAELKPVFQ 143
Db 81 LDQRDDGNEIQAVLGEMTGSRTVPRCFIDGKFVGSGTDVKRLVEQG----ILOKYFQ 133

RESULT 5
US-09-270-767-47604
; Sequence 47604, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 47604
LENGTH: 137
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-47604

Query Match 27.5%; Score 196.5; DB 2; Length 137;
Best Local Similarity 37.6%; Pred. No. 1.8e-15;
Matches 44; Conservative 26; Mismatches 36; Indels 11; Gaps 4;

QY 30 LSTPKMVSQETVAH---VKDLIGOKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLE 86
DB 25 LQPTLVSDSSHAQFVRTISGNKVIFSKVCPYC-SWAKEQFRKINV---KATVIE 80
QY 87 LDEMSNGSETQDALEISGQKTVPNVYINGKHIGNSDLETLLKNGKLAELKPVFQ 143
DB 81 LDQRDDGNEIQAVLGEMTGRTPRCFIDGKFVGGGTDVKRLYEQG----ILQKYFQ 133

RESULT 6
US-09-248-796A-18114
Sequence 18114, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: 107196.132
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US/09/248,796A
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18114
LENGTH: 60
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-18114

Query Match 24.4%; Score 174; DB 2; Length 60;
Best Local Similarity 57.9%; Pred. No. 2.6e-13;
Matches 33; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 84 VLELDENSGSETQDALEISGQKTVPNVYINGKHIGNSDLETLLKNGKLAELK 140
DB 3 ILBELDEVDDGAEIQEALLEITGQRTVENVFIGGHGNSDVAQALNSIDLNKKFKP 59

RESULT 7
US-09-621-976-5130
Sequence 5130, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm

SEQ ID NO 5130
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-5130

Query Match 24.2%; Score 173; DB 2; Length 114;
Best Local Similarity 36.7%; Pred. No. 8.8e-13;
Matches 36; Conservative 22; Mismatches 36; Indels 4; Gaps 2;

QY 41 VAHVKDLIGOKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLELDENSGSEI 100
DB 17 VNOIQETISDNCVIFSKTSCSYC-TWAKKLFHDMNV---NYKVVELDLLEYGNQF 72
QY 101 EETSQKTVPNVYINGKHIGNSDLETLLKNGKLAEL 138
DB 73 YKMTGERTVPRIFVNGTFFIGGATDTHRLHKEGKLPLV 110

RESULT 8
US-08-911-319A-1
Sequence 1, Application US/08911319A
Patent No. 5968798
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,319A
FILING DATE: August 14, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Muenzen, Colette C.
REGISTRATION NUMBER: 39,784
REFERENCE/DOCKET NUMBER: PF-0363 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THPLNOT03
CLONE: 2447829
US-08-911-319A-1

Query Match 24.2%; Score 173; DB 1; Length 164;
Best Local Similarity 36.7%; Pred. No. 1.5e-12;
Matches 36; Conservative 22; Mismatches 36; Indels 4; Gaps 2;

QY 41 VAHVKDLIGOKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLELDENSGSEI 100
DB 57 VNOIQETISDNCVIFSKTSCSYC-TWAKKLFHDMNV---NYKVVELDLLEYGNQF 112

Qy 101 EBSGQKTPNVVINGKHGNSDLETLKKGKLAETL 138
Db 113 YKMTGERTVPRIFVNGTFIGGATDTHRLHKEGKLLPLV 150

RESULT 9

US-09-352-619-1
; Sequence 1, Application US/09352619
; Patent No. 6084070
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/352,619
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,319
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Muenzen, Colette C.
; REGISTRATION NUMBER: 39,784
; REFERENCE/DOCKET NUMBER: PF-0363 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 164 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPINOT03
; CLONE: 2447829
US-09-352-619-1

Query Match 24.2%; Score 173; DB 2; Length 164;
Best Local Similarity 36.7%; Pred. No. 1.5e-12;
Matches 36; Conservative 22; Mismatches 36; Indels 4; Gaps 2;

Qy 41 VAHVXDLIGQKEVFAAKTCYCKATLSTLFQELNVPKSKALVLELDMSGSEIQDAL 100
Db 57 VNQIQETISDNCVWIFSKTSCSYC-TMAKKLFHDMNV---NYKVVLDLLEYGNGQFDAL 112

Qy 101 EBSGQKTPNVVINGKHGNSDLETLKKGKLAETL 138
Db 113 YKMTGERTVPRIFVNGTFIGGATDTHRLHKEGKLLPLV 150

RESULT 10

US-09-162-564-3
; Sequence 3, Application US/09162564
; Patent No. 6379664
; GENERAL INFORMATION:
; APPLICANT: Lou, Marjorie
; APPLICANT: Raghavachari, Nalini
; APPLICANT: Qiao, Fengyu
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR THE PREVENTION AND TREATMENT

; TITLE OF INVENTION: OF OXIDATIVE DAMAGE IN OCULAR TISSUES
; FILE REFERENCE: UNL-98-2-1
; CURRENT APPLICATION NUMBER: US/09/162,564
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-162-564-3

Query Match 21.2%; Score 151.5; DB 2; Length 106;
Best Local Similarity 35.3%; Pred. No. 3e-10;
Matches 36; Conservative 24; Mismatches 37; Indels 5; Gaps 2;
Qy 42 AHVXDLIGQKEVFAAKTCYCKATLSTLFQELNVPKSKALV--LELDMSGSEIQDA 99
Db 4 AFVNSKIOPGVVFIKPTCFCKTKOELLQ--LPFKEGLLEFVDITATSDTNEIQDY 60
Qy 100 LBEISGQKTPNVVINGKHGNSDLETLKKGKLAETL 141
Db 61 LQQLTGARTVPRVFIGKICIGGCTDLESMHKEGELLRLQOI 102

RESULT 11

US-09-621-976-5132
; Sequence 5132, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5132
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-5132

Query Match 20.4%; Score 146; DB 2; Length 94;
Best Local Similarity 37.0%; Pred. No. 1.1e-09;
Matches 30; Conservative 19; Mismatches 28; Indels 4; Gaps 2;

Qy 41 VAHVXDLIGQKEVFAAKTCYCKATLSTLFQELNVPKSKALVLELDMSGSEIQDAL 100
Db 17 VNQIQETISDNCVWIFSKTSCSYC-TMAKKLFHDMNV---NYKVVLDLLEYGNGQFDAL 72

Qy 101 EBSGQKTPNVVINGKHG 121

Db 73 YKMTGERTVPRIFVNGTFIGG 93

RESULT 12

US-09-162-564-5
; Sequence 5, Application US/09162564
; Patent No. 6379664
; GENERAL INFORMATION:
; APPLICANT: Lou, Marjorie
; APPLICANT: Raghavachari, Nalini
; APPLICANT: Qiao, Fengyu
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR THE PREVENTION AND TREATMENT
; FILE REFERENCE: UNL-98-2-1
; CURRENT APPLICATION NUMBER: US/09/162,564
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-162-564-5

Query Match      20.2%; Score 145; DB 2; Length 105;
Best Local Similarity 37.4%; Pred. No. 1.8e-09;
Matches 37; Conservative 18; Mismatches 40; Indels 4; Gaps 2;

QY 42 AHVKDLIGQKEVFVAAKTYPYCKATLSTLFOELNVPKSKAL-VLELDENSGSEIQDAL 100
Db 4 AFVNSKIQPKGVVFIKPTCPYCKRQELLSQ---LPFKQLLEFVDITATSDN 60

QY 101 EISGQKTPNVYINGKHIGGNSDLETLKNGKLAELIK 139
Db 61 QQLTGARTVPRVFIGQECIGGCTDLVNMHGERGELLTRLK 99

RESULT 13
US-09-162-564-6
; Sequence 6, Application US/09162564
; Patent No. 6379664
; GENERAL INFORMATION:
; APPLICANT: Lou, Marjorie
; APPLICANT: Raghavachari, Nalini
; APPLICANT: Qiao, Fengyu
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR THE PREVENTION AND TREATMENT
; TITLE OF INVENTION: OF OXIDATIVE DAMAGE IN OCULAR TISSUES
; FILE REFERENCE: UNL-98-2-1
; CURRENT APPLICATION NUMBER: US/09/162,564
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-162-564-6

Query Match      20.2%; Score 144.5; DB 2; Length 107;
Best Local Similarity 36.7%; Pred. No. 2.1e-09;
Matches 36; Conservative 20; Mismatches 37; Indels 5; Gaps 2;

QY 44 VKDLIGQKEVFVAAKTYPYCKATLSTLFOELNVPKSKALV--LELDENSGSEIQDAL 101
Db 6 VNSKIQPKGVVFIKPTCPYCKRQELLSQ---LPFKQLLEFVDITATSDN 62

QY 102 EISGQKTPNVYINGKHIGGNSDLETLKNGKLAELIK 139
Db 63 QLTGARTVPRVFIGKDCIGGCSDLIAMQEKGLLARLK 100

RESULT 14
US-09-162-564-2
; Sequence 2, Application US/09162564
; Patent No. 6379664
; GENERAL INFORMATION:
; APPLICANT: Lou, Marjorie
; APPLICANT: Raghavachari, Nalini
; APPLICANT: Qiao, Fengyu
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR THE PREVENTION AND TREATMENT
; TITLE OF INVENTION: OF OXIDATIVE DAMAGE IN OCULAR TISSUES
; FILE REFERENCE: UNL-98-2-1
; CURRENT APPLICATION NUMBER: US/09/162,564
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-162-564-2

Query Match      20.2%; Score 144; DB 2; Length 106;
Best Local Similarity 35.2%; Pred. No. 2.4e-09;
Matches 38; Conservative 27; Mismatches 35; Indels 8; Gaps 4;

QY 36 VSQETVAHVKDLIGQKEVFVAAKTYPYCKATLSTLFOELNVPKSKALV--LELDENSG 93
Db 1 MAQEFV-NCKIQPKGVVFI--KPTCPYCKRQELLSQ---LPFKQLLEFVDITATSDT 54

QY 94 SEIQDALEISGQKTPNVYINGKHIGGNSDLETLKNGKLAELIKPV 141
Db 55 NEIQDYLOQLTGARTVPRVFIGKDCIGGCTDLVNMHGERGELLTRLQOI 102

RESULT 15
US-08-911-319A-3
; Sequence 3, Application US/08911319A
; Patent No. 5988798
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,319A
; FILING DATE: August 14, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Muenzen, Colette C.
; REGISTRATION NUMBER: 39,784
; REFERENCE/DOCKET NUMBER: PF-0363 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-845-4166
; TELEFAX: 650-855-0555
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 531405
US-08-911-319A-3

Query Match      20.0%; Score 143; DB 1; Length 106;
Best Local Similarity 35.2%; Pred. No. 3.1e-09;
Matches 38; Conservative 27; Mismatches 35; Indels 8; Gaps 4;

QY 36 VSQETVAHVKDLIGQKEVFVAAKTYPYCKATLSTLFOELNVPKSKALV--LELDENSG 93
Db 1 MAQEFV-NCKIQPKGVVFI--KPTCPYCKRQELLSQ---LPFKQLLEFVDITATSDT 54

QY 94 SEIQDALEISGQKTPNVYINGKHIGGNSDLETLKNGKLAELIKPV 141
Db 55 NEIQDYLOQLTGARTVPRVFIGKDCIGGCSDLVLSQSGELLTRLQOI 102
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Search completed: November 6, 2006, 19:18:51
Job time : 54 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2006, 03:23:26 ; Search time 451 Seconds
(without alignments)
6678.517 Million cell updates/sec

Title: US-10-523-362-3
Perfect score: 432
Sequence: 1 atggagacaaatttttcctt.....tgaagcgggtatttcaatag 432

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*
15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	432	100.0	432	12	ADK90658 Baker's Y
2	432	100.0	432	13	ADT87074 Yeast Str
3	432	100.0	932	6	ABQ76354 S. cerevi
4	147.4	34.1	833	6	ABQ76320 S. cerevi
5	143.4	33.2	333	12	ADK90656 Baker's Y
6	89	20.6	360	6	ABQ76591 C. albica
7	89	20.6	360	6	ABZ32493 Candida a
8	64.6	15.0	621	2	ADK02454 A. gossyp
9	57.8	13.4	440	8	ABZ53183 Aspergill
10	56	13.0	531	11	ACL32590 Rice abio
11	55.6	12.9	733	12	ADK90702 Rice oxid
12	55.2	12.8	619	3	AAC43844 Arabidops
13	55	12.7	278	7	ADS70498 Corn seed
14	55	12.7	392	14	ABE65134 Rice geno
15	55	12.7	628	12	ADK90700 Rice oxid
16	54.8	12.7	309	13	ADR85786 Aspergill
17	54.8	12.7	336	12	ADK90680 Thale cre
18	54.8	12.7	378	3	AAC48716 Arabidops

19	54.8	12.7	608	3	AAC32667 Arabidops
20	54.8	12.7	636	3	AAC48717 Arabidops
21	54.4	12.6	594	3	AAC44274 Arabidops
22	53.2	12.3	628	3	AAC40081 Arabidops
23	53.2	12.3	657	12	ADK90670 Rape oxid
24	51.2	11.9	7337	13	ADR84319 Aspergill
25	50	11.6	540	12	ADK90688 Thale cre
26	50	11.6	707	3	AAC47504 Arabidops
27	50	11.6	709	3	AAC34109 Arabidops
28	49.2	11.4	512	6	ABK71699 Human dit
29	49.2	11.4	621	13	ADK33976 Plant ful
30	49.2	11.4	864	13	ADK50598 Plant ful
31	46.8	10.8	385	12	ADP92474 Cotton ex
32	46.8	10.8	590	13	ACN53628 Cotton an
33	46.4	10.7	529	12	ADP91617 Cotton ex
34	45.6	10.6	446	4	ABL13599 Drosophil
35	45.6	10.6	478	4	ABL11847 Drosophil
36	45.6	10.6	2446	4	ABL13598 Drosophil
37	45.4	10.5	672	12	ADK90674 Rape oxid
38	45	10.4	550	13	ACN61980 Cotton gy
39	44.8	10.4	479	5	AAH87770 Peppermin
40	44.6	10.3	832	13	ADT19470 Plant CDN
41	44	10.2	302	10	ABX85625 Corn ear-
42	44	10.2	535	11	ACL30824 Rice abio
43	43.8	10.1	343	13	ACN49246 Cotton pr
44	43.8	10.1	501	5	AAH87771 Peppermin
45	43.8	10.1	546	13	ACN47600 Cotton pr

ALIGNMENTS

RESULT 1
ADK90658
ID ADK90658 standard; cDNA; 432 BP.

XX AC ADK90658;

DT 20-MAY-2004 (first entry)

XX DE Baker's yeast glutaredoxin 2 (GRX2) cDNA SeqID 3.

XX KW baker's yeast; GRX2; gene; ss; transgenic; abiotic stress response;
crop plant; oxidoreductase stress-related protein; ORSRP;
environmental stress; salinity; drought; temperature; chemical; pathogen;
glutaredoxin; GRX; thioredoxin; THX; Quantitative Trait Locus; QTL.

XX KW Saccharomyces cerevisiae.

XX OS WO2004018687-A2.

XX PN 04-MAR-2004.

XX PF 01-JUL-2003; 2003WO-EP006994.

XX PR 07-AUG-2002; 2002EP-00017671.

XX PA (BADI) BASF PLANT SCI GMBH.

XX PI Chardonnais A, Puzio P;

XX DR WPI; 2004-226856/21.

XX DR P-PSDB; ADK90659.

XX PT New transgenic plant cell transformed by oxidoreductase stress-related
protein (ORSRP) coding nucleic acid, useful for producing a transgenic
plant with increased environmental stress tolerance.

XX PS Claim 5; SEQ ID NO 3; 140pp; English.

XX CC This invention relates to novel transgenic plant cells transformed by
genes encoding proteins associated with the abiotic stress response.
Specifically, it refers to transgenic crop plants expressing the

CC heterologous oxidoreductase stress-related protein (ORSRP) that confers increased tolerance and/or resistance to environmental stresses such as salinity, drought, temperature, chemicals or pathogens. The present invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/or thioredoxin (TRX) proteins, where expression is under the control of an inducible tissue-specific or developmentally-specific promoter and CC furthermore it provides antisense oligos and RNA interference molecules CC to inhibit ORSRP expression. In addition, these nucleic acids are useful CC as Quantitative Trait Locus (QTL) markers that can map genetic loci CC associated with environmental stress tolerance. This polynucleotide CC sequence is a baker's yeast GRX cDNA of the invention.

SQ Sequence 432 BP; 142 A; 81 C; 85 G; 124 T; 0 U; 0 Other;

Query Match 100.0%; Score 432; DB 12; Length 432;
Best Local Similarity 100.0%; Pred. NO. 4e-112;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGACCAATTTTCCTTCGACTCGAATTTAAATTTGTTATTATCATTCACGTTGTTT 60
Db 1 ATGGAGACCAATTTTCCTTCGACTCGAATTTAAATTTGTTATTATCATTCACGTTGTTT 60

Qy 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGAAACA 120
Db 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGAAACA 120

Qy 121 GTTGCTCAGTAAGATCTGATGGCCAAAGAAAGTGTGTTGTCAGCAAGACATAC 180
Db 121 GTTGCTCAGTAAGATCTGATGGCCAAAGAAAGTGTGTTGTCAGCAAGACATAC 180

Qy 181 TSCCCTTACTGAAGCTACTTGTCTACCCCTCTCCAGAAATGACGTTCCCAATCC 240
Db 181 TSCCCTTACTGAAGCTACTTGTCTACCCCTCTCCAGAAATGACGTTCCCAATCC 240

Qy 241 AAGCCCTTGTGTGGAAATAGATGAATGAGCAATGGCTCAGAGATTCAGACGCTTTA 300
Db 241 AAGCCCTTGTGTGGAAATAGATGAATGAGCAATGGCTCAGAGATTCAGACGCTTTA 300

Qy 301 GAAGAAATCTGGGCCAAAACCTGTACCTAACGATACATCAATGCGCAAGCATTTGGT 360
Db 301 GAAGAAATCTGGGCCAAAACCTGTACCTAACGATACATCAATGCGCAAGCATTTGGT 360

Qy 361 GGTAAACGCAATTTGGAACTTTGAGAAAATGGCAAGTACGTGAAATATTGAAGCCG 420
Db 361 GGTAAACGCAATTTGGAACTTTGAGAAAATGGCAAGTACGTGAAATATTGAAGCCG 420

Qy 421 GTATTTCAATAG 432
Db 421 GTATTTCAATAG 432

RESULT 2
ADT87074
ID ADT87074 standard; DNA; 432 BP.
XX AC ADT87074;
XX AC ADT87074;
XX 13-JAN-2005 (first entry)
XX Yeast Stress-related protein gene YEL045C.
XX Yeast; Stress-related protein; SRP; ds; gene; environmental stress;
XX abiotic stress; drought; heat; cold; salt.
XX Saccharomyces cerevisiae.
XX W02004092398-A2.
XX 28-OCT-2004.
XX 15-APR-2004; 2004WO-US011888.
XX 15-APR-2003; 2003EP-00008080.
PR

PR 02-MAY-2003; 2003BP-00039728.
PR 01-AUG-2003; 2003EP-00016672.
XX 30-SEP-2003; 2003EP-00022225.
PA (BADI) BASF PLANT SCI GMBH.
XX Puzio P, Chardonnens A, Shirley A, Wang X, Sarria-Millan R;
PI Mckersie B, Chen R;
XX WPI; 2004-766883/75.
DR P-PSDB; ADT87075.
XX
PT New isolated nucleic acid molecule comprises a sequence encoding Stress-Related Protein (SRP), useful for producing transformed plants with altered metabolic activity resulting in increased tolerance or resistance to environmental stress.
PT
XX Claim 20; SEQ ID NO 52; 911pp; English.
XX
CC The invention relates an isolated nucleic acid molecule comprises a nucleic acid molecule encoding a Stress-Related Protein (SRP), from Yeast or E. coli and their homologues from Rice, Soybean and Rape. Also included are a transformed plant cell with altered metabolic activity compared to a corresponding non-transformed wild type plant cell (where the metabolic activity is altered by transformation with a SRP coding nucleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell), a transgenic plant generated from the plant cell above (and which is a monocot or dicot plant, or a gymnosperm plant), a seed produced by a transgenic plant above (where the seed is genetically homozygous for a transgene conferring altered metabolic activity resulting in an increased tolerance to environmental stress as compared to a corresponding non-transformed wild type plant), a nucleic acid construct which confers the expression of the nucleic acid molecule above (comprising one or more regulatory elements, where expression of the SRP coding nucleic acid in a host cell results in altered metabolic activity resulting in increased tolerance to environmental stress as compared to a corresponding non-transformed wild type host cell), a vector comprising the nucleic acid molecule above or the nucleic acid construct, a host cell which has been transformed stably or transiently with the vector (or the nucleic acid molecules above, or the nucleic acid construct), an isolated Stress Related Protein (SRP) selected from the amino acid sequences fully given in the specification and/or its homologues, a method of producing a transgenic plant with altered metabolic activity compared to a corresponding non-transformed wild type plant cell, modifying stress tolerance of a plant, detecting environmental stress in plant cells or plants, screening plant cells or plants for increased tolerance and/or resistance to environmental stress, breeding plant cells or plants towards increased tolerance and/or resistance to environmental stress, increasing tolerance of a plant to at least one abiotic stress, a plant transformed with the nucleic acids above and a seed of the plant, The altered metabolic activity and/or a SRP encoding nucleic acids or its homologues are useful as markers for selection of plants or plant cells with increased tolerance to environmental stress, or for detection of stress in plants or plant cells. The nucleic acids are useful for producing transformed plants with altered metabolic activity resulting in increased tolerance and/or resistance to an environmental stress (drought, heat, cold and salt) as compared to a corresponding non-transformed wild-type plant cell. The present sequence is a yeast gene encoding an SRP of the invention.

XX
SQ Sequence 432 BP; 142 A; 81 C; 85 G; 124 T; 0 U; 0 Other;

Query Match 100.0%; Score 432; DB 13; Length 432;
Best Local Similarity 100.0%; Pred. NO. 4e-112;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGACCAATTTTCCTTCGACTCGAATTTAAATTTGTTATTATCATTCACGTTGTTT 60
Db 1 ATGGAGACCAATTTTCCTTCGACTCGAATTTAAATTTGTTATTATCATTCACGTTGTTT 60
Qy 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGAAACA 120
Db 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGAAACA 120
Qy 121 GTTGCTCAGTAAGATCTGATGGCCAAAGAAAGTGTGTTGTCAGCAAGACATAC 180
Db 121 GTTGCTCAGTAAGATCTGATGGCCAAAGAAAGTGTGTTGTCAGCAAGACATAC 180
Qy 181 TSCCCTTACTGAAGCTACTTGTCTACCCCTCTCCAGAAATGACGTTCCCAATCC 240
Db 181 TSCCCTTACTGAAGCTACTTGTCTACCCCTCTCCAGAAATGACGTTCCCAATCC 240
Qy 241 AAGCCCTTGTGTGGAAATAGATGAATGAGCAATGGCTCAGAGATTCAGACGCTTTA 300
Db 241 AAGCCCTTGTGTGGAAATAGATGAATGAGCAATGGCTCAGAGATTCAGACGCTTTA 300
Qy 301 GAAGAAATCTGGGCCAAAACCTGTACCTAACGATACATCAATGCGCAAGCATTTGGT 360
Db 301 GAAGAAATCTGGGCCAAAACCTGTACCTAACGATACATCAATGCGCAAGCATTTGGT 360
Qy 361 GGTAAACGCAATTTGGAACTTTGAGAAAATGGCAAGTACGTGAAATATTGAAGCCG 420
Db 361 GGTAAACGCAATTTGGAACTTTGAGAAAATGGCAAGTACGTGAAATATTGAAGCCG 420
Qy 421 GTATTTCAATAG 432
Db 421 GTATTTCAATAG 432

Db 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCGAGAAACA 120
Qy 121 GTTGCTCAGTAAGGATCTGATTTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 180
Db 121 GTTGCTCAGTAAGGATCTGATTTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 180
Qy 181 TGGCTTACTGTAAGACTGTTGTCCTACCTCTTCCAGAAATGAACGTTCCCAATCC 240
Db 181 TGGCTTACTGTAAGACTGTTGTCCTACCTCTTCCAGAAATGAACGTTCCCAATCC 240
Qy 241 AAGGCTTCTGTTGGAAATAGATGAATGCAATGGCTCAGAGATTCAGACGCTTTA 300
Db 241 AAGGCTTCTGTTGGAAATAGATGAATGCAATGGCTCAGAGATTCAGACGCTTTA 300
Qy 301 GAAGAAATCTCGGCGCCAAAACCTGTACCTAAGCTATACATCAATGCGCAAGCATTTGGT 360
Db 301 GAAGAAATCTCGGCGCCAAAACCTGTACCTAAGCTATACATCAATGCGCAAGCATTTGGT 360
Qy 361 GGTACAGCGATTTGGAACCTTTGAGAAAAATGGCAAGTTAGCTGAAATATTTGAAGCCG 420
Db 361 GGTACAGCGATTTGGAACCTTTGAGAAAAATGGCAAGTTAGCTGAAATATTTGAAGCCG 420
Qy 421 GTATTTCATAG 432
Db 421 GTATTTCATAG 432
RESULT 3
ABQ76354
ID ABQ76354 standard; cDNA; 932 BP.
XX AC ABQ76354;
XX DT 21-NOV-2002 (first entry)
XX DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 133.
XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KW neurodegeneration; cell death; ss.
XX Saccharomyces cerevisiae.
XX WO200264766-A2.
XX 22-AUG-2002.
XX 21-DEC-2001; 2001WO-EP015398.
XX 22-DEC-2000; 2000EP-00870318.
XX 04-JAN-2001; 2001EP-00870002.
XX 09-JAN-2001; 2001EP-00870003.
XX (JANC) JANSSEN PHARM NV.
XX Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;
XX WPI; 2002-667002/71.
XX P-PSDB; ABG93088.
XX New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medicament for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.
XX Claim 36; Fig 1; 344pp; English.
XX This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or

CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide; immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenic flora of humans and
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polynucleotide associated with the Bax gene
CC described in the disclosure of the invention
XX
SQ Sequence 932 BP; 270 A; 220 C; 158 G; 284 T; 0 U; 0 Other;
Query Match 100.0%; Score 432; DB 6; Length 932;
Best Local Similarity 100.0%; Pred. No. 5.1e-112;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGAGACCAATTTTCTTCGACTCGAATTTAAATGTTTATTATCATCATCAGTGTGTTT 60
Db 501 ATGGAGACCAATTTTCTTCGACTCGAATTTAAATGTTTATTATCATCATCAGTGTGTTT 560
Qy 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCGAGAAACA 120
Db 561 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCGAGAAACA 620
Qy 121 GTTGCTCAGTAAGGATCTGATTTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 180
Db 621 GTTGCTCAGTAAGGATCTGATTTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 680
Qy 181 TGGCTTACTGTAAGACTGTTGTCCTACCTCTTCCAGAAATGAACGTTCCCAATCC 240
Db 681 TGGCTTACTGTAAGACTGTTGTCCTACCTCTTCCAGAAATGAACGTTCCCAATCC 740
Qy 241 AAGGCTTCTGTTGGAAATAGATGAATGCAATGGCTCAGAGATTCAGACGCTTTA 300
Db 741 AAGGCTTCTGTTGGAAATAGATGAATGCAATGGCTCAGAGATTCAGACGCTTTA 800
Qy 301 GAAGAAATCTCGGCGCCAAAACCTGTACCTAAGCTATACATCAATGCGCAAGCATTTGGT 360
Db 801 GAAGAAATCTCGGCGCCAAAACCTGTACCTAAGCTATACATCAATGCGCAAGCATTTGGT 860
Qy 361 GGTACAGCGATTTGGAACCTTTGAGAAAAATGGCAAGTTAGCTGAAATATTTGAAGCCG 420
Db 861 GGTACAGCGATTTGGAACCTTTGAGAAAAATGGCAAGTTAGCTGAAATATTTGAAGCCG 920
Qy 421 GTATTTCATAG 432
Db 921 GTATTTCATAG 932
RESULT 4
ABQ76320
ID ABQ76320 standard; cDNA; 833 BP.
XX AC ABQ76320;
XX DT 21-NOV-2002 (first entry)
XX DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 65.
XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KW neurodegeneration; cell death; ss.
XX Saccharomyces cerevisiae.
XX WO200264766-A2.

Qy 283 GAGATTCAAGACGCTTTAGAGAAATCTCGGGCAAAACTGTACTTAACGTATACATC 342
Db 181 GACATTGAGCTGCTGTTATATGAGATTAAATGGCAAGAACCGTGGCAAAATCTATATT 240
Qy 343 AATGGCAAGCACATTGCTGCTTAACAGCGATTTCGAACTTTGAGAAATGCGCAAGTTA 402
Db 241 AATGGTAAACATATTGGAGCAACGACGACTTGAGGAATTGAGGAGACTGCTGTAATTG 300
Qy 403 GCTGAATATTGAAGCGGCTATTTCATA 431
Db 301 GAGGAATTGTTAGAACCTATTCTTGCAAA 329

RESULT 6
ABQ76591
ID ABQ76591 standard; cDNA; 360 BP.
AC ABQ76591;
XX
DT 21-NOV-2002 (first entry)
XX
DE C. albicans BAX-associated cDNA fragment SEQ ID 607.
XX
XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KW neurodegeneration; cell death; ss.
XX
OS Candida albicans.
XX
PN WO200264766-A2.
XX
PD 22-AUG-2002.
XX
PF 21-DEC-2001; 2001WO-EP015398.
XX
PR 22-DEC-2000; 2000EP-00870318.
PR 04-JAN-2001; 2001EP-00870002.
PR 09-JAN-2001; 2001EP-00870003..
XX
PA (JANC) JANSSEN PHARM NV.
XX
XX Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;
XX
XX WPI; 2002-667002/71.
DR P-PSDB; ABG93325.
XX
XX New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medicament for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.
XX
PS Claim 36; Fig 2; 344pp; English.
XX
XX This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi; identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide, immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenous flora of humans and
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polynucleotide associated with the Bax gene

CC described in the disclosure of the invention
XX
SQ Sequence 360 BP; 129 A; 68 C; 62 G; 101 T; 0 U; 0 Other;
Query Match 20.6%; Score 89; DB 6; Length 360;
Best Local Similarity 55.4%; Pred.No. 5.6e-15;
Matches 201; Conservative 0; Mismatches 150; Indels 12; Gaps 1;
Qy 67 AGAATATTGCTAAAGATTTTATCTACTCCAAAATGGTATCCAGGAACAGTTGCT 126
Db 10 ACATTATTAAACCAAGAGACTATTTCATATACATCAACAATGGTTTCATCTCAAGTTAAGAAC 69
Qy 127 CAGTAAAGATCTGATGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATACCTGCT 186
Db 70 AAGTCAACAATTTGATCAAAACCAACCAAGTTTTCATTTGCTCCAAATCCTATTGTCCA 129
Qy 187 TACTGTAAAGTACTTTTGTCTACCTCTTCCAAAGATTGAAAGTTCCCAATCCAAGGCC 246
Db 130 TACTGTAAAGTACTTACCAAAAGCAC-----AATTGAAGCTATTAACAAGGATGCT 177
Qy 247 CTTGCTTTGGAATTAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAA 306
Db 178 TACATTTCTGAAATTAGACGAGTTGACGACGGTCTGAAATCCAAAGACATTTATTGGAA 237
Qy 307 ATCTCGGCAAAAACCTGTACTTAACGTATACATCAATCAATGGCAAGCACATTTGTTGTAAC 366
Db 238 ATCACTGGTCAAAAGAACCGTTCCAAATGCTTTTATTGGTGGTCAACATATTGGTGGCAAT 297
Qy 367 AGCGATTTGGAACCTTTGAAGAAATGCAAGTTAGCTGAAATATTGAAGCGGTTATTT 426
Db 298 TCGATGTGCAAGCTTTGAAGTCTAGTGACAAATTAGATGACAAAATCAAAGCTGCTTTA 357
Qy 427 CAA 429
Db 358 TAA 360

RESULT 7
ABZ32493
ID ABZ32493 standard; DNA; 360 BP.
XX
AC ABZ32493;
XX
DT 30-JAN-2003 (first entry)
XX
DE Candida albicans essential gene SEQ ID NO 6780.
XX
KW Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal; gene; ss.
XX
OS Candida albicans.
XX
PN WO200253728-A2.
XX
PD 11-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-US049486.
XX
PR 29-DEC-2000; 2000US-0259128P.
PR 20-FEB-2001; 2001US-00792024.
PR 22-AUG-2001; 2001US-0314050P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
PI
XX WPI; 2002-566694/60.
DR P-PSDB; ABP73943.
XX
XX Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.

```
XX Claim 37; SEQ ID NO 6780; 167pp + Sequence Listing; English.
PS The invention relates to constructing (M1) a strain of diploid fungal
XX cells in which both alleles of a gene are modified, comprising modifying
XX one allele by insertion or replacement by a cassette having an
XX expressible selectable marker and modifying other allele by
XX recombination, of a promoter replacement fragment with a heterologous
XX promoter, so that expression of the second allele is regulated by the
XX promoter. (M1) is useful for constructing a strain of diploid fungal
XX cells in which both alleles of a gene are modified. The diploid fungal
XX cells having both alleles modified are useful for identifying a gene that
XX is essential to the survival or growth of a fungus, a gene that
XX contributes to the virulence and/or pathogenicity of a fungus, a gene
XX that contributes to the resistance of a diploid fungus to an antifungal
XX agent, an antifungal agent that inhibits the growth of a diploid fungal
XX and for identifying a therapeutic agent for treatment of a mammalian
XX disease. (M1) is useful for identifying a compound which modulates the
XX activity of a gene product, preferably enzymatic activity, carbon
XX compound catabolism, biosynthetic, transporter, transcriptional,
XX translational, signal transduction, DNA replication and cell division
XX activity. The method is useful for identifying a compound having the
XX ability to inhibit growth or proliferation of C. albicans cells and for
XX treating infection by C. albicans. The present sequence is that of an
XX essential Candida albicans gene used in the method of the invention.
XX Note: The sequence data for this patent is not represented in the printed
XX specification but is based on sequence information supplied to Derwent by
XX the European Patent Office
SQ Sequence 360 BP; 129 A; 68 C; 62 G; 101 T; 0 U; 0 Other;

Query Match 20.6%; Score 89; DB 6; Length 360;
Best Local Similarity 55.4%; Pred. No. 5.6e-15;
Matches 201; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

QY 67 AGAATTATTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCGAGGAAACAGTTGCT 126
DB 10 ACATTATTACCAAGAGACTATTCAATACATCAACATGTTTCATCTCAAGTTAAGNAC 69

QY 127 CAGCTAAAGATCTGATGGCCAAAAGGAAGTGTTGTTGTCAGCAAGACATATGCGCCT 186
DB 70 AAGGTCCGAACAATTGATCAAAAACCAACACAGTTTTCATTGCTCCAAATCCTATTGTCCA 129

QY 187 TACTGTAAGCTACTTGTGCTACCTCTTCCAGATTGAACTTCCCAATCCAAGGCC 246
DB 130 TACTGTAAGCTACCAAAAGCAC-----AATTGAAGCTATAACAAGGATGCT 177

QY 247 CTGTGTGTGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAAGMA 306
DB 178 TACATCTTGATTAGACGAAGTTGACGAGCGTGTGAATCCAGNAGCATTTTGGAA 237

QY 307 ATCTCGGGCCAAAACCTGACTACCTAAGTATATACATCAATGGCAAGCACATTTGGTGAAC 366
DB 238 ATCACTGGTCAAGAACCGTTCCAAATGTCTTTATTGGTGGTCAACATATTTGGTGGCAAT 297

QY 367 AGCGATTGCAAACTTTGAAGAAAAATGGCAAGTAGCTAGCTGAATATTTGAAGCCGGTATT 426
DB 298 TCCGATGTGAAGCTTTGAAGTCTAGTGACAAATTTAGATGACAAAATCAAAAGCTGCTTTA 357

QY 427 CAA 429
DB 358 TAA 360

RESULT 8
ADRO2454
ID ADRO2454 standard; DNA; 621 BP.
XX AC ADRO2454;
XX AC
XX XX
XX 23-SEP-2004 (first entry)
XX XX
XX A. gossypii genomic DNA PAG1696UP.
```

```
XX Filamentous funghi; ds; forensic identification; gene characterisation;
KW intergenomic comparison; chromosome mapping.
XX Eremothecium gossypii.
OS US6239264-B1.
PN 29-MAY-2001.
XX PD
XX 24-DEC-1997; 97US-00998416.
XX PF
XX 31-DEC-1996; 97CH-00000016.
XX PR
XX (SYNG-) SYNGENTA PARTICIPATIONS AG.
PA
XX Philippaen P, Poeschlmann R, Steiner-Lange S, Mohr C, Wendland J;
PI Knechtle P, Rebischung C;
XX WPI; 1998-388120/33.
XX
XX New gene for adenylate cyclase from Ashbya gossypii - useful for
PT generating recombinant microorganisms with alteration in gene of cAMP-
PT dependent signalling pathway for increasing production of fine chemicals.
XX
XX Example 3; SEQ ID NO 1146; 632pp; English.
PS
XX The invention relates to isolated DNA molecules comprising isolated
XX genomic DNA sequences from the filamentous funghi Ashbya gossypii, the
XX sequences comprising ADRO1309, ADRO1366, ADRO1367, ADRO1388, ADRO1428,
XX ADRO1466, ADRO1629, ADRO1637, ADRO2057, ADRO2345 and ADRO2369, chosen
XX from 1047 disclosed genomic sequences. Also included is a cloning vector
XX comprising a nucleotide sequence chosen from the above sequences. The
XX novel Ashbya gossypii genomic sequences are useful for forensic
XX identification, gene characterisation, for studying gene organisation by
XX intergenomic comparison (with Saccharomyces cerevisiae), identifying
XX biosynthetic genes for selectable markers, to isolate
XX promoters/terminators/centromeres, chromosome mapping, and in identifying
XX sequences unique to Ashbya gossypii for species identification. The
XX present sequence is an A. gossypii novel genomic sequence of the
XX invention.
XX
XX Sequence 621 BP; 137 A; 177 C; 179 G; 128 T; 0 U; 0 Other;

Query Match 15.0%; Score 64.6; DB 2; Length 621;
Best Local Similarity 55.0%; Pred. No. 5.4e-08;
Matches 149; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 100 AAAATGGTATCCAGGAAACAGTTGCTCAGCTAAAGGATCTGATGGCCAAAGGAAGTG 159
DB 350 ATAAATGGTTTCCCTTCGGTTATTAAACAGGTGCGCGCTAATCCAGCAGAACCGCGTG 409

QY 160 TTTGTTGACGAGAAAGACATACCTGCTTACTGTAAGCTACTTTGTCTACCTCTTTCCAA 219
DB 410 TTCAATGTCATCAAGACGCTACTGTCCGTATTGCCAGGCGCAAGCGTACGTTGCTGGAG 469

QY 220 GAATTGAAGCTTCCAAATCCAAAGGCCCTTGTGTTGGAATTAGATGAATAGCAAT--- 276
DB 470 GAGAAGCGCGTCCCGCAGCGCAGTAAACCTGTTGGAGCTTGACACCATCGGCGAGGAG 529

QY 277 GGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCGGGCCAAAACCTCTACTTAACGTA 336
DB 530 GCGCGCGGTATCCAAAGCGCGTTCAGGAGCTGAGCGGCGAGCGGACCGTGCCCAATC 589

QY 337 TACATCAATGGCAAGCACATTTGGTGTAACTA 367
DB 590 TACATCAAGCGGCGCATGCTGGGTGCAACA 620

RESULT 9
ABZ53183
ID ABZ53183 standard; cDNA; 440 BP.
XX
```

```
AC ABZ53183;
XX
XX 28-MAR-2003 (first entry)
XX
XX Aspergillus oryzae polynucleotide SEQ ID NO 2296.
XX
XX Aspergillus oryzae; fermentation; fungus; industrial; EST;
KW expressed sequence tag; gene; ss.
XX
XX Aspergillus oryzae.
XX
XX WO200279476-A1.
XX
XX 10-OCT-2002.
XX
XX 22-MAR-2002; 2002WO-IB000890.
XX
XX 30-MAR-2001; 2001JP-00098371.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (NARE-) NAT RES INST BREWING.
XX (NORQ) NAT FOOD RES INST MIN AGRIC.
XX
XX Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;
PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;
XX
XX WPI; 2003-046817/04.
XX
XX
XX Detection of expression of specific Aspergillus genes for monitoring the
PT fermentation and growth conditions of the fungus, using DNA probes.
XX
XX Claim 1; SEQ ID NO 2296; 48pp + Sequence Listing; Japanese.
XX
XX The invention relates to a polynucleotide having any of 6006 specific
CC sequences (ABZ5088-ABZ5693), which are expressed by a fungus under
CC specific culture conditions including one or more of eutrophic,
CC oligotrophic, solid, early germination, alkaline, high temperature, low
CC temperature or maltose culture or polynucleotides stringently hybridising
CC to these sequences. The polynucleotides are useful for monitoring the
CC progress of fermentation and the growth conditions of a fungus,
CC especially of Aspergillus oryzae which is widely used in industrial
CC fermentation. Also monitoring for fungal contamination. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 440 BP; 101 A; 139 C; 100 G; 100 T; 0 U; 0 Other;
SQ
Query Match 13.4%; Score 57.8; DB 8; Length 440;
Best Local Similarity 55.3%; Pred. No. 4.1e-06;
Matches 141; Conservative 0; Mismatches 102; Indels 12; Gaps 1;
QY 134 AGGATCTGATTGGCCAAAGGAAGTGTGTGTGTCAGCAAGACATATCGCCCTTACTGTGA 193
DB 103 AGGGCATCATCAAGCCCAAGCCGCTGCTGCTTTCTTCCAAAGTCTACTGGCCCTACTGCA 162
QY 194 AAGCTACTTTGTCTACCTCTTCCAAAGATTTGAAGCTTCCCAATCCAGGCCCTTGTGT 253
DB 163 AATCTAGCAAGAGCGCTCTCTTAGCCA-----GCTGGAGCAAGTACCTCACC 210
QY 254 TGGAAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTTGAAGAATAATCTCGG 313
DB 211 TCGAGCTCGATGAAGAGCGGATGGCAGGCCATCCAGAGCGCTCTGTGGAATCAGCG 270
QY 314 GCCAAAAAATGTACTTAACGTATATCATCAATGGCAAGCAATTTGGTGGTAACAGCGATT 373
DB 271 GCCAGCGCACGCTCCCAACATTTTCATCAAGCAGAGCATATCGTGGGAATCTCGGATC 330
QY 374 TGGAACTTTTGAAGA 388
DB 331 TGCAGGCTCGCAAAA 345
```

```
RESULT 10
AC ACL32590
ID ACL32590 standard; cDNA; 531 BP.
XX
XX ACL32590;
AC
XX 02-JUN-2005 (first entry)
DT
XX Rice abiotic stress response related polynucleotide SEQ ID NO:11153.
DE
XX ss; abiotic stress tolerance; transgenic plant; plant; cereal;
KW agriculture.
XX
XX Oryza sativa.
OS
XX WO2003008540-A2.
PN
XX 30-JAN-2003.
PD
XX 21-JUN-2002; 2002WO-US019668.
XX
XX 22-JUN-2001; 2001US-0300112P.
XX
XX 24-AUG-2001; 2001US-0314662P.
PR
XX 26-SEP-2001; 2001US-0325277P.
PR
XX 21-NOV-2001; 2001US-0332132P.
PR
XX (SVGN) SYNGENTA PARTICIPATIONS AG.
PA
XX
XX Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX
XX WPI; 2003-248011/24.
DR
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Disclosure; SEQ ID NO 11153; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
XX Sequence 531 BP; 122 A; 111 C; 145 G; 153 T; 0 U; 0 Other;
SQ
Query Match 13.0%; Score 56; DB 11; Length 531;
Best Local Similarity 58.3%; Pred. No. 1.4e-05;
Matches 98; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 254 TGGAAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAAGAAATCTCGG 313
DB 141 TTGAGTTGGACACTGAAGCGGATGGAATTCAGATTCAGTCAGCTCTTGCTGAATGGACTG 200
QY 314 GCCAAAAAATGTACTTAACGTATATCATCAATGGCAAGCAATTTGGTGGTAACAGCGATT 373
DB 201 GGCAGAGGAGCTGTTCCTCAATGTCTTCAATCAATGAAAAACACATTTGGTGGCTGTGACGATA 260
QY 374 TGGAAACTTTGAAGAAAAATGGCAATTTAGCTGAATATTTGAAGCCGG 421
DB 261 CTATTGCACTGAACAAGGGAGGGAAGCTGTTGCTCTGCTGACGGAGG 308
```


RESULT 11

ADK90702
ID ADK90702 standard; cDNA; 733 BP.

XX AC
XX ADK90702;

XX AC
XX 20-MAY-2004 (first entry)

XX DE
XX Rice oxidoreductase stress-related protein cDNA OZ1116C2194 SeqID 47.

XX KW rice; gene; ss; transgenic; abiotic stress response; crop plant;
KW oxidoreductase stress-related protein; ORSRP; environmental stress;
KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
KW thioredoxin; THX; Quantitative trait locus; QTL.

XX OS
XX Oryza sativa.

XX PN
XX WO2004018687-A2.

XX PD
XX 04-MAR-2004.

XX XX
XX 01-JUL-2003; 2003WO-EP006994.

XX XX
XX 07-AUG-2002; 2002EP-00017671.

XX XX
XX (BADI) BASF PLANT SCI GMBH.

XX XX
XX Chardonnais A, Puzio P;

XX PI
XX WPI; 2004-226856/21.

XX DR
XX P-PSDB; ADK90703.

XX PT
XX New transgenic plant cell transformed by oxidoreductase stress-related
XX protein (ORSRP) coding nucleic acid, useful for producing a transgenic
XX plant with increased environmental stress tolerance.

XX PS
XX Claim 5; SEQ ID NO 47; 140pp; English.

XX CC This invention relates to novel transgenic plant cells transformed by
XX genes encoding proteins associated with the abiotic stress response.
XX Specifically, it refers to transgenic crop plants expressing the
XX heterologous oxidoreductase stress-related protein (ORSRP) that confers
XX increased tolerance and/or resistance to environmental stresses such as
XX salinity, drought, temperature, chemicals or pathogens. The present
XX invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/ or
XX thioredoxin (THX) proteins, where expression is under the control of an
XX inducible tissue-specific or developmentally-specific promoter and
XX furthermore it provides antisense oligos and RNA interference molecules
XX to inhibit ORSRP expression. In addition, these nucleic acids are useful
XX as Quantitative Trait Locus (QTL) markers that can map genetic loci
XX associated with environmental stress tolerance. This polynucleotide
XX sequence is a rice ORSRP cDNA of the invention.

XX SQ
XX Sequence 733 BP; 222 A; 176 C; 166 G; 169 T; 0 U; 0 Other;

Query Match 12.9%; Score 55.6; DB 12; Length 733;

Best Local Similarity 60.7%; Pred. No. 2e-05;

Matches 91; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 254 TGGATTAGTAAGTAATGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCGG 313

Db 258 TTGAGTTGGATGGGGAGTGATGGATCTCAGCTGCAGTCGGCACTTGCTGAATGACTG 317

QY 314 GCCAAAAAAGTGTACCTAAAGTATACATCAATGGCAAGCACATTGGTGGTAACAGCGATT 373

Db 318 GACAAAGGATGTTCCAAATGTCTTATCAATGGGAGCATATTGGTGGCTGTGATGATA 377

QY 374 TGGAAACTTTGAAGAAAAATGGCAAGTTAG 403

Db 378 CTTTGGCATTGAACAAATGAAGGGAAGCTGG 407

RESULT 12

AAC43844

ID AAC43844 standard; DNA; 619 BP.

XX AC
XX AAC43844;

XX DT
XX 18-OCT-2000 (first entry)

XX DE
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 40715.

XX KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

XX OS
XX Arabidopsis thaliana.

XX PN
XX EP1033405-A2.

XX PD
XX 06-SEP-2000.

XX XX
XX 25-FEB-2000; 2000EP-00301439.

XX PR
XX 25-FEB-1999; 99US-0121825P.

XX PR
XX 05-MAR-1999; 99US-0123180P.

XX PR
XX 09-MAR-1999; 99US-0123548P.

XX PR
XX 23-MAR-1999; 99US-0125788P.

XX PR
XX 25-MAR-1999; 99US-0126264P.

XX PR
XX 29-MAR-1999; 99US-0126785P.

XX PR
XX 01-APR-1999; 99US-0127462P.

XX PR
XX 08-APR-1999; 99US-0128234P.

XX PR
XX 16-APR-1999; 99US-0128714P.

XX PR
XX 19-APR-1999; 99US-0129845P.

XX PR
XX 21-APR-1999; 99US-0130077P.

XX PR
XX 23-APR-1999; 99US-0130449P.

XX PR
XX 23-APR-1999; 99US-0130510P.

XX PR
XX 28-APR-1999; 99US-0130891P.

XX PR
XX 30-APR-1999; 99US-0131449P.

XX PR
XX 30-APR-1999; 99US-0132048P.

XX PR
XX 04-MAY-1999; 99US-0132407P.

XX PR
XX 05-MAY-1999; 99US-0132484P.

XX PR
XX 06-MAY-1999; 99US-0132485P.

XX PR
XX 06-MAY-1999; 99US-0132486P.

XX PR
XX 07-MAY-1999; 99US-0132487P.

XX PR
XX 11-MAY-1999; 99US-0132633P.

XX PR
XX 14-MAY-1999; 99US-0132566P.

XX PR
XX 14-MAY-1999; 99US-0134218P.

XX PR
XX 14-MAY-1999; 99US-0134219P.

XX PR
XX 18-MAY-1999; 99US-0134370P.

XX PR
XX 18-MAY-1999; 99US-0134768P.

XX PR
XX 19-MAY-1999; 99US-0134941P.

XX PR
XX 20-MAY-1999; 99US-0135124P.

XX PR
XX 21-MAY-1999; 99US-0135353P.

XX PR
XX 24-MAY-1999; 99US-0135629P.

XX PR
XX 25-MAY-1999; 99US-0136021P.

XX PR
XX 27-MAY-1999; 99US-0136392P.

XX PR
XX 28-MAY-1999; 99US-0136782P.

XX PR
XX 01-JUN-1999; 99US-0137222P.

XX PR
XX 03-JUN-1999; 99US-0137528P.

XX PR
XX 04-JUN-1999; 99US-0137502P.

XX PR
XX 07-JUN-1999; 99US-0137724P.

XX PR
XX 08-JUN-1999; 99US-0138094P.

XX PR
XX 10-JUN-1999; 99US-0138540P.

XX PR
XX 10-JUN-1999; 99US-0138847P.

XX PR
XX 14-JUN-1999; 99US-0139119P.

XX PR
XX 16-JUN-1999; 99US-0139452P.

XX PR
XX 16-JUN-1999; 99US-0139453P.

XX PR
XX 17-JUN-1999; 99US-0139492P.

XX PR
XX 18-JUN-1999; 99US-0139454P.

XX PR
XX 18-JUN-1999; 99US-0139455P.

XX PR
XX 18-JUN-1999; 99US-0139456P.

XX PR
XX 18-JUN-1999; 99US-0139457P.

XX PR
XX 18-JUN-1999; 99US-0139458P.

XX PR
XX 18-JUN-1999; 99US-0139459P.

RESULT 13

AD570498
ID AD570498 standard; cDNA; 278 BP.
XX
AC AD570498;
XX
DT 18-NOV-2004 (first entry)
XX
DE Corn seedling-derived polynucleotide (cpds), SEQ ID 5514.
XX
XX Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth;
XX seed development; disease resistance; insect infestation; fungal disease;
XX bacterial infection; Goss' Bacterial Wilt; blight; bacterial leaf blight;
XX Stewart's Bacterial Wilt; Holcus spot; bacterial leaf blight; leaf spot;
XX bacterial stripe; maize dwarf mosaic virus infection;
XX environmental stress; water stress; pH stress; temperature stress;
XX pollution; injury; pesticide.
XX
OS Zea mays.
XX
PN US2003237110-A9.
XX
PD 25-DEC-2003.
XX
PF 06-AUG-2001; 2001US-00923876.
XX
PR 12-MAY-1998; 98US-0085331P.
XX
PR 21-APR-1999; 99US-00298329.
XX
XX (INCY-) INCYTE PHARM INC.
XX
PI Lalgudi RV, Ito LY, Sherman BK;
XX
DR WPI; 2002-195165/25.
XX
XX New corn seedling-derived polynucleotides and polypeptides, useful in
XX identifying and altering desired characteristics associated with growth
XX and development, disease resistance, environmental adaptability, quality
XX and yield.
XX
PS Claim 1; SEQ ID NO 5514; 33pp; English.

XX
XX The invention relates to a corn seedling-derived polynucleotide (cdp)
XX selected from ADS64985-ADS71316, or their complements and fragments. Also
XX included are a composition for the detection of altered expression of a
XX cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a
XX method of detecting a polynucleotide in a biological sample using a cdp,
XX a method for using oligomers (and amplification) to recover a regulatory
XX element from a DNA library using oligomers designed against a cdp, a
XX seedling specific regulatory element that regulates the expression of a
XX cdp, an expression vector containing a cdp or regulatory element, a plant
XX transformed with the vector, a host cell containing the vector (and
XX expressing a corn seedling derived protein, CDP), an anti-CDP antibody,
XX identifying a compound which binds a CDP and screening a plurality of
XX compounds for binding to cdp polynucleotide. The cdp polynucleotides,
XX proteins, vectors, cells and antibodies are useful for the
XX identification, evaluation and alteration of seed growth and development,
XX disease resistance (e.g. to insect infestation, fungal disease, bacterial
XX infection, Goss' Bacterial Wilt, blight, Stewart's Bacterial Wilt, Holcus
XX spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf
XX mosaic virus infection) and resistance to environmental stress (e.g.
XX water stress, pH stress, temperature stress, pollution, injury or
XX pesticides. The present sequence is cdp cDNA sequence.

SQ Sequence 278 BP; 74 A; 56 C; 77 G; 71 T; 0 U; 0 Other;

Query Match 12.7%; Score 55; DB 7; Length 278;

Best Local Similarity 57.1%; Pred. No. 2.2e-05;
Matches 100; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 242 AGGCCCTTGTTGGATTAGATGAAATGAGCAATGCTCAGAGATTCAGAGCGCTTTAG 301

, Db 77 AGCCATATGTTGGAGCTTGATCAGGAGGAGTGGCTCAGAGATTCAGATTCGCTTAC 136

QY 302 AAGAAATCTCGGGCCAAAAAACTGTACCTAAGTATACATCAATGCAAGCACATTGGTG 361
DB 137 TTGAGATAGTTGGCAGGCGTACTGTGCTCCCTCAAGTTTTTTCATGGAAGCACCTGGTG 196
QY 362 GTAACAGCGATTGTGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAATATTGAA 416
DB 197 GTTCTGACGATGACTGTTGACTCTCTAGGAAGTGGAAAACTGGCTAGACTTCTAAA 251

RESULT 14

AE65134
ID AE65134 standard; DNA; 392 BP.
XX
AC AE65134;
XX
DT 22-SEP-2005 (first entry)
XX
DE Rice genome derived DNA sequence, SEQ ID 279.

XX
XX transcription; gene regulation; transgenic plant; RNA interference;
XX transformation; antibody; ds.
XX
OS Oryza sp.
XX
PN JP2005185101-A.
XX
PD 14-JUL-2005.
XX
PF 11-DEC-2002; 2002JP-00383870.
XX
PR 30-MAY-2002; 2002JP-00203269.

XX
XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.
XX (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
XX (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.

XX Kikuchi H, Hayashizaki Y, Otomo Y, Matsubara K, Murakami K;
XX Kishimoto N, Sato K, Nagata T, Kawakami N, Yazaki J, Ishikawa M;
XX Doi K, Kawai J;

XX WPI; 2005-566181/58.

XX
XX Novel DNA encoding transcription factor, derived from rice plant, useful
XX for obtaining transcriptional-regulatory regions in plant and for
XX producing modified plant.
XX
PS Claim 1; SEQ ID NO 279; 2928pp; Japanese.

XX
XX The invention relates to a novel DNA sequence encoding a transcription
XX factor derived from a plant. The invention further comprises antisense
XX RNA sequences, ribozyme activity RNA, RNAi sequences, a vector,
XX transformed plant cells, antibodies and proteins, all related to the
XX novel plant DNA sequences of the invention. The novel DNA is preferably
XX derived from a rice-genome database. The invention further provides a
XX method for determining the transcription regulatory regions of the rice
XX genome. The novel DNA is useful for controlling the expression of a gene
XX in a plant and for producing a modified plant with desired and different
XX characteristics. The plant DNA and method enables the acquisition of many
XX transcriptional-regulatory regions. This polynucleotide represents a DNA
XX sequence taken from a rice genome clone library for use in the invention.
XX Note: This sequence is not shown in the specification. It has been
XX retrieved from a sequence listing in electronic format from the Japanese
XX Patent Office. The invention claims DNA sequences of SEQ ID Nos 1 to
XX 28469 and encoded protein sequences of SEQ ID Nos 28470 to 56791,
XX however, the sequence listing only provided the DNA sequences of SEQ ID
XX Nos 1 to 3032.

SQ Sequence 392 BP; 112 A; 75 C; 91 G; 114 T; 0 U; 0 Other;

Query Match 12.7%; Score 55; DB 14; Length 392;

Best Local Similarity 57.1%; Pred. No. 2.5e-05;

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2006, 03:33:13 ; Search time 4440 Seconds
(without alignments)

5440.800 Million cell updates/sec

Title: US-10-523-362-3

Perfect score: 432

Sequence: 1 atggagaccaatttttcctt.....tgaagcgggtatttcaatag 432

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gse1:*
12: gb_gse2:*
13: gb_gse3:*
14: gb_gse4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	346.8	80.3	969	14	CNS06HAM
C 2	241.8	56.0	390	10	T36608
C 3	221	51.2	307	10	T36930
C 4	164	38.0	902	14	CNS06KVC
5	137.6	31.9	920	14	CNS075L8
6	137.6	31.9	997	14	CNS073AT
7	124.6	28.8	966	14	CNS075E3
C 8	99.6	23.1	434	11	AZ925612
C 9	94	21.8	420	10	T37408
C 10	90.6	21.0	454	11	AZ926128
C 11	72.4	16.8	848	13	CZ286838
C 12	68.8	15.9	492	9	DN156309
C 13	68.4	15.8	529	8	CN813116
C 14	68	15.7	522	8	CN813786
C 15	67.6	15.6	477	5	CD459632
C 16	66.6	15.4	504	9	DN156705
C 17	66.4	15.4	772	13	CZ289630
C 18	66	15.3	405	3	BP520191
C 19	66	15.3	435	3	BP520391

20	66	15.3	762	8	CV182757
C 21	65.2	15.1	381	2	BJ955512
C 22	65.2	15.1	388	2	BJ953571
C 23	65.2	15.1	433	2	BJ942895
C 24	65.2	15.1	435	2	BJ953134
C 25	65.2	15.1	452	5	CD457966
C 26	65.2	15.1	472	2	BJ942458
C 27	65.2	15.1	501	2	BJ961669
C 28	65.2	15.1	526	2	BJ950022
C 29	65.2	15.1	532	2	BJ950704
C 30	65.2	15.1	548	2	BJ167220
C 31	65.2	15.1	548	2	BJ950490
C 32	65.2	15.1	552	2	BJ950702
C 33	65.2	15.1	559	2	BJ941223
C 34	65	15.0	433	3	BP508298
C 35	63.6	14.7	583	8	CO214935
C 36	63.6	14.7	586	8	CO208264
C 37	63.2	14.6	783	1	AL669647
C 38	63	14.6	405	2	BJ944737
C 39	63	14.6	477	8	CN811635
C 40	61.4	14.2	272	2	BJ961436
C 41	61.4	14.2	332	2	BJ961671
C 42	61.4	14.2	368	2	BJ960957
C 43	61.4	14.2	372	2	BJ951802
C 44	60.6	14.0	657	5	CF867737
C 45	60.6	14.0	779	4	CB897783

ALIGNMENTS

RESULT 1
CNS06HAM

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

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JOURNAL

PUBLISHED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

CNS06HAM 969 bp DNA linear GSS 17-AUG-2005
T7 end of clone AS0AA011A12 of library AS0AA from strain CLIB 533
of Saccharomyces bayanus, genomic survey sequence.

AL398756

AL398756.1 GI:12152529

GSS.

Saccharomyces uvarum

Saccharomyces uvarum

Saccharomycetales; Saccharomycetaceae; Saccharomycetes;

1 (bases 1 to 969)

Souciot J., Aigle M., Artiguenave F., Blandin G.,

Bolotin-Fukuhara M., Bon E., Brottier P., Casaregola S., de

Montigny J., Dujon B., Durand P., Gaillardin C., Lepingle A.,

Llorente B., Malpertuy A., Neuvéglise C., Ozier-Kalogeropoulos O.,

Potier S., Saurin W., Tekai F., Toffano-Nioche C.,

Wesolowski-Louvel M., Wincker P., and Weissenbach J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

yeast species for molecular evolution studies

FEBS Lett. 487 (1), 3-12 (2000)

11152876

2 (bases 1 to 969)

Bon E., Neuvéglise C., Casaregola S., Artiguenave F., Wincker P.,

Aigle M., and Durand P.

Genomic exploration of the hemiascomycetous yeasts: 5.

Saccharomyces bayanus var. uvarum

FEBS Lett. 487 (1), 37-41 (2000)

11152880

3 (bases 1 to 969)

Genoscope.

Direct Submission

Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :

seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen

yeast species: Saccharomyces bayanus var. uvarum, Saccharomycetes

exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces

lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia

angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,

Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES	LOCATION/Qualifiers	ORIGIN
source	1..969 /organism="Saccharomyces uvarum" /mol_type="genomic DNA" /strain="CLIB 533" /cultivar="uvarum" /db_xref="taxon:230603" /clone="AS0AA011A12" /clone_lib="AS0AA" /notes="end : T7"	Query Match 80.3%; Score 346.8; DB 14; Length 969; Best Local Similarity 87.5%; Pred. No. 3.6e-84; Matches 378; Conservative 1; Mismatches 53; Indels 0; Gaps 0;
misc_feature	<68..>496 /inference="non-experimental evidence, no additional details recorded"	
misc_feature	/notes="similar to Saccharomyces cerevisiae ORF YDR513w [TTR1; glutaredoxin 1]" /inference="non-experimental evidence, no additional details recorded" /notes="similar to Saccharomyces cerevisiae ORF YDR514c [strong similarity to hypothetical protein YCL036w]"	
ORIGIN		
QY	1 ATGGAGACCAATTTTTCCTCGACTCGAATTTAATTTATTTATTCATTATCAGTTGTTT 60	
DB	68 ATGGAGACTAATTTTCTTCGACTCGAATTTAATCGTTATTCATTATCAGTTGTTT 127	
QY	61 GCCACAAGAAATATTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGAAACA 120	
DB	128 GCCACAGAAATATTGCTAAAGATTTTATCTACTCCAAAATGGTATCTCAAGAAACA 187	
QY	121 GTTGCTCAGTAAAGGACTTGATTGGCCAAAAGAAAGTGTGTTGTCAGCAAGACATAC 180	
DB	188 ATTGCACACGTAAAGGACTTGATTGGCCAAAAGAGGCTCTCGTTGCCGCCGAAGACATAC 247	
QY	181 TGCCTTACTGTAAAGTACTTGTCTACCTCTTCCAGAATTTGAACGTTCCCAATCC 240	
DB	248 TGTCTTACTGTAAAGCACAATGTCCACTTGTTCAGGAATTTGAACGTTCTCAATCT 307	
QY	241 AAGCCCTCTGTGTGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTA 300	
DB	308 AAAGCCGTGTTGTTGGATTGGAGAAATGAGCAATGGTTCAAGATTCAGATGCTCTC 367	
QY	301 GAAGAAATCTCGGCCCAAAAACTGTACCTAACGTATACATCAATGGCAAGCACATGGT 360	
DB	368 GAAGAAATTTCCGGCCAGAAAACCGTACCACAAACGTTTATATCAATGGAAGCACATCGGT 427	
QY	361 GGTAAACGCAATTTGGAACCTTTGAGAAAAAATGGCAAGTTAGTGAATATTGAAGCCG 420	
DB	428 GGTAAACGCAATTTGGAAGCTTTGAAGAAAAACGGTAAGTTGGCTGAATATTGAAGCCG 487	
QY	421 GTATTTCATAG 432	
DB	488 GKTTTGAATAG 499	
RESULT 2		
LOCUS	T36608	
DEFINITION	EST101575 S. cerevisiae strain X2180-1A Saccharomyces cerevisiae cDNA 3' end, mRNA sequence.	
ACCESSION	T36608	
VERSION	T36608.1	
KEYWORDS	EST.	
SOURCE	Saccharomyces cerevisiae (baker's yeast)	
ORGANISM	Saccharomyces cerevisiae	

REFERENCE	AUTHORS	ORIGIN
JOURNAL	TITLE	
COMMENT	Unpublished (1995)	
Other ESTs: TC20		
Contact: Weinstein, K. and Venter, J. C.		
The Institute for Genomic Research		
932 Clopper Rd, Gaithersburg, MD 20878		
Tel: 3018699056		
Fax: 3018699423		
Email: tdbinfo@db.tigr.org		
For clone availability please contact the TIGR Database		
(tdbinfo@db.tigr.org)		
Seq primer: M13-21.		
FEATURES	Location/Qualifiers	
source	1..390 /organism="Saccharomyces cerevisiae" /mol_type="mRNA" /strain="X2180-1A" /db_xref="taxon:4932" /clone_lib="S. cerevisiae strain X2180-1A" /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"	
Query Match	56.0%; Score 241.8; DB 10; Length 390;	
Best Local Similarity	97.1%; Pred. No. 2.2e-55;	
Matches	299; Conservative 0; Mismatches 3; Indels 6; Gaps 5;	
QY	131 TAAAGATCTGATTGGCC--AAAAGGAAGTGTGTTGTCAGCAAG-ACATACTG-CCCT 186	
DB	390 TAAAGGATCTGATTGGCCCAAAAGGAAGTGTGTTGTCAGCAAGACATACCTGCCCCCT 331	
QY	187 TACTGTAAAGTACTTTGTCTACCTCTTCCAAAGATTGAAGCTTCCCAAAT-CCAAGGC 245	
DB	330 TACTGTAAAGTACTTTGTCTACCTCTTCCAAAGATTGAAGCTTCCCAAATCCAAGGC 271	
QY	246 CTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAGA 305	
DB	270 CTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAGA 211	
QY	306 AATCTCGGCC-AAAAACTGTACCTTAAGTATACATCAATGCGAAGCACATTGGTGTA 364	
DB	210 AATCTCGGCCCAAAAAACTGTACCTTAAGTATACATCAATGCGAAGCACATTGGTGTA 151	
QY	365 ACAGCGATTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAAAATATTGAAGCCGTTAT 424	
DB	150 ACAGCGATTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAAAATATTGAAGCCGTTAT 91	
QY	425 TTCAATAG 432	
DB	90 TTCAATAG 83	
RESULT 3		
LOCUS	T36930/c	
DEFINITION	EST101959 S. cerevisiae strain X2180-1A Saccharomyces cerevisiae cDNA 3' end, mRNA sequence.	
ACCESSION	T36930	
VERSION	T36930.1	
KEYWORDS	EST.	
SOURCE	Saccharomyces cerevisiae (baker's yeast)	
ORGANISM	Saccharomyces cerevisiae	
REFERENCE	AUTHORS	
JOURNAL	TITLE	
COMMENT	Unpublished (1995)	
Other ESTs: TC20		

Contact: Weinstock,K. and Venter,J.C.
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability please contact the TIGR Database
(tdbinfo@db.tigr.org)
Seq primer: M13-21.

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FEATURES
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        1..307
        /organism="Saccharomyces cerevisiae"
        /mol_type="mRNA"
        /strain="X2180-1A"
        /db_xref="taxon:4932"
        /clone_lib="S. cerevisiae strain X2180-1A"
        /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
    Query Match      51.2%; Score 221; DB 10; Length 307;
    Best Local Similarity 98.2%; Pred. No. 1.1e-49;
    Matches 221; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 208 ACCCTCTTCCAGAAATGGAACGTTCCCAATCCAAAGCCCTTGTGTTGGAATTAGATGAA 267
Db 307 ACCCTCTTCCAGAAATGGAACGTTCCCAATCCAAAGCCCTTGTGTTGGAATTAGATGAA 248

Qy 268 ATGAGCAATGGCTCAGAGATTCAGAGCGTTTGAAGAAATCTCGGCCCAAAAACTGTA 327
Db 247 ATGAGCAATGGCTCAGAGATTCAGAGCGTTTGAAGAAATCTCGGCCCAAAAACTGTA 188

Qy 328 CCTAACGTATACATCAATGCAAGCACATTTGGTGTAAACAGCGATTTGGAACCTTTGAAG 387
Db 187 CCTAACGTATACATCAATGCAAGCACATTTGGTGTAAACAGCGATTTGGAACCTTTGNAG 128

Qy 388 AAAAAATGGCAAGTTAGCTGAATATTTGAAGCCGTTATTTCAATAG 432
Db 127 NAAATGGCAAGTTAGTGNATATTTGAAGCCGTTATTTCAATAG 83

RESULT 4
LOCUS CENS06KYC 902 bp DNA linear GSS 17-JUN-2001
DEFINITION T7 end of clone AT0AA009A07 of library AT0AA from strain CBS 4311
of Saccharomyces servazzii, genomic survey sequence.
ACCESSION AL403498
VERSION AL403498.1 GI:12163814
KEYWORDS GSS.
SOURCE Saccharomyces servazzii
ORGANISM Saccharomyces servazzii
REFERENCE 1 (bases 1 to 902)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durand,P., Lepingle,A., Llorente,B.,
Maupertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FBES Lett. 487 (1), 3-12 (2000)
11152876
2 (bases 1 to 902)
AUTHORS Casaregola,S., Lepingle,A., Bon,E., Neuveglise,C., Nguyen,H.,
Artiguenave,F., Wincker,P. and Gaillardin,C.
Genomic exploration of the hemiascomycetous yeasts: 7.
Saccharomyces servazzii
11152882
3 (bases 1 to 902)
AUTHORS Genoscope.

```

```

TITLE Direct Submission
JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
FEATURES
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        /mol_type="genomic DNA"
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        /db_xref="taxon:27293"
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        /clone_lib="AT0AA"
        /note="end : T7"
        complement (<153..>503)
        /inference="non-experimental evidence, no additional
        details recorded"
        /notes="similar to Saccharomyces cerevisiae ORF YDR513w [
        TFR1 ; glutaredoxin ]"

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        38.0%; Score 164; DB 14; Length 902;
        Best Local Similarity 66.3%; Pred. No. 6.7e-34;
        Matches 236; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

ORIGIN
    Query Match      38.0%; Score 164; DB 14; Length 902;
    Best Local Similarity 66.3%; Pred. No. 6.7e-34;
    Matches 236; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

Qy 77 CTAAGAATTTTATCTACTCCAAAATGGTATCCAGGAAACAGTGTCTCAGTAAGG 136
Db 499 CTAACAAATTTTATTACTCAGAAAATGGTCTCTCAAGCTACTATCAACACGTCAAAG 440

Qy 137 ATCTGATTGGCCAAAGGAAGTGTGTTGTCAGCAAGACATCTGCGCTTACTGTAAAG 196
Db 439 AATTAAATGCTGAAGAAGATATTTTCATTCCTTCAAGACTTACTGTCCATCTGCTG 380

Qy 197 CTACTTTGTCTACCCCTCTTCCAAAGAAATGAACGTTCCCAATCCAAAGCCCTTGTGTGG 256
Db 379 CCACCTTTAAGACTGTGTTCAAGAGACCTTAAACGCTCCTGAATCCAAAGCTGCTGTTAC 320

Qy 257 AATTAGATGAATGAGCAATGGCTCAGAGATTCAGACGCTTTAGAGAAATCTCGGGCC 316
Db 319 AATTAGATGAATGAGTATGATGGTGGCCGAAATTCAGGAAGCTTTGAAGGAAATTACTGGTC 260

Qy 317 AAAAACTGTACCTTACCTATACATCAATGGCAAGCACATTTGTTGTTAAGCGGATTTGG 376
Db 259 AATCTACCGTCCCAAAACACTTTTCATTAACGTCACACATTTGGTGGTATGACATCTAC 200

Qy 377 AAACCTTTGAAGAAAAATGGCAAGTGTAGCTGAATATTTGAAGCCGCTTATTTCAATAG 432
Db 199 AAACCTTTGAAGAACTCTGTTAGTGTAGACTCTTTATTAAAGGATGCTCTAGCTTAG 144

RESULT 5
LOCUS CENS075L8 920 bp DNA linear GSS 07-JUL-2001
DEFINITION clone BA0AB036E06 of library BA0AB from strain CL1B 210 of
Kluyveromyces lactis, genomic survey sequence.
ACCESSION AL430242
VERSION AL430242.1 GI:12213436
KEYWORDS GSS.
SOURCE Kluyveromyces lactis
ORGANISM Kluyveromyces lactis
REFERENCE 1 (bases 1 to 920)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,

```


Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Maupertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissbach, J.

TITLE
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL
PUBMED
11152876

REFERENCE
2 (bases 1 to 920)
Bolotin-Fukuhara, M., Toffano-Nioche, C., Artiguenave, F., Duchateau-Nguyen, G., Lemaire, M., Marmeisse, R., Montrocher, R., Robert, C., Termier, M., Wincker, P. and Wesolowski-Louvel, M.

TITLE
Genomic exploration of the hemiascomycetous yeasts: 11.

JOURNAL
PUBMED
11152886

REFERENCE
3 (bases 1 to 920)
Genoscope.

TITLE
Direct Submission

JOURNAL
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
source
1..920
/organism="Kluyveromyces lactis"
/mol_type="genomic DNA"
/strain="CLIB 210"
/variety="lactis"
/db_xref="taxon:28985"
/clone="BA0AB036E06"
/clone_lib="BA0AB"
447..>806
/inference="non-experimental evidence, no additional details recorded"
/notes="similar to Saccharomyces cerevisiae ORF YDR513w [TTR1 ; Glutaredoxin]"

misc_feature
513..>806
/inference="non-experimental evidence, no additional details recorded"
/notes="similar to Saccharomyces cerevisiae ORF YCL035c [GRX1 ; Glutaredoxin]"

ORIGIN

Query Match 31.9%; Score 137.6; DB 14; Length 920;
Best Local Similarity 63.1%; Pred. No. 1.2e-26;
Matches 212; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Qy 89 TATCTACTCCAAAATGGTATCCAGGAAACAGTTGCTACAGTAAAGGATCTGATGGCC 148
Db 499 TACATCTTTCAAAATGCCAAGTGGCGCACATCGCTGTGTCACAGGTTTAACTCACT 558
Qy 149 AAAAGGAAGTGTGTGTGTCAGCAAGACATACCTGCCCTTACTGTAAAGCTACTTGTCTA 208
Db 559 CATCTAAGATCTTTGTCGCTTCAAAGACATCTGTCATCTGCCAAGCCACTTTGAAA 618
Qy 209 CCCTCTCCAGAAATGAAGCTTCCCAATCCAGGCCCTTGTGTGGAATTAGATGAAA 268
Db 619 CTTTGTGTTGAAGAAAGAAAGAGTGGACAAAAGTTGGCTACTGTTTTCGAATTGAACCAAC 678
Qy 269 TGAGCAATGCTCAGAGATTCAAGACGCTTTAGAGAATACTCGGGCCAAAACACTGTAC 328
Db 679 TAGAAGATGTTTCGATATTTCAGATGCTTTGGCAGAAATTACCGGCCAAAAGACTGTTC 738

Qy 329 CTAACGTATACATCAATGCGAAGCACATTTGGTGGTAACAGCGATTTGGAACCTTCAAGA 388
Db 739 CAAACATCTTTTAAATGTTGTTGCGAAGCACATCGGTGGTAACCTCTGATTTGCAAGAGTTGAACA 798

Qy 389 AAAATGGCAAGTTAGCTGAATATATTGAAGCCGGTAT 424
Db 799 ACTCGGTGATTGGTAAGTTGTTGGCTTCCTTAT 834

RESULT 6
LOCUS CNS073AT
DEFINITION clone BA0AB018B12 of library BA0AB from strain CLIB 210 of Kluyveromyces lactis, genomic survey sequence.
ACCESSION AL427275
VERSION AL427275.1 GI:12210469
KEYWORDS GSS.
SOURCE Kluyveromyces lactis
ORGANISM Kluyveromyces lactis

REFERENCE
AUTHORS Souciet, J.-L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Maupertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissbach, J.

TITLE
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL
PUBMED
11152876

REFERENCE
2 (bases 1 to 997)
Bolotin-Fukuhara, M., Toffano-Nioche, C., Artiguenave, F., Duchateau-Nguyen, G., Lemaire, M., Marmeisse, R., Montrocher, R., Robert, C., Termier, M., Wincker, P. and Wesolowski-Louvel, M.

TITLE
Genomic exploration of the hemiascomycetous yeasts: 11.

JOURNAL
PUBMED
11152886

REFERENCE
3 (bases 1 to 997)
Genoscope.

TITLE
Direct Submission

JOURNAL
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
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1..997
/organism="Kluyveromyces lactis"
/mol_type="genomic DNA"
/strain="CLIB 210"
/variety="lactis"
/db_xref="taxon:28985"
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/clone_lib="BA0AB"
563..>922
/inference="non-experimental evidence, no additional details recorded"
/note="similar to Saccharomyces cerevisiae ORF YDR513w [TTR1 ; Glutaredoxin]"
4629..>922
/inference="non-experimental evidence, no additional details recorded"

misc_feature
563..>922
/inference="non-experimental evidence, no additional details recorded"
/note="similar to Saccharomyces cerevisiae ORF YDR513w [TTR1 ; Glutaredoxin]"
4629..>922
/inference="non-experimental evidence, no additional details recorded"

Tel: 314 362 2735
Fax: 314 362 7855

Email: mj@genetics.wustl.edu
Class: random plasmid subclone.

FEATURES

source
1. .434
/organism="Saccharomyces paradoxus"
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/clone="4910.e234c13.81"
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/note="Random genomic sequence"

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Query Match 23.1%; Score 99.6; DB 11; Length 434;
Best Local Similarity 64.6%; Pred. No. 2.9e-16;
Matches 164; Conservative 0; Mismatches 89; Indels 1; Gaps 1;
QY 64 ACAAGAATTATGCTAAAGATTTTATCTACTCCAAAATGATGATCCGA-GGAACAGT 122
DB 254 ATACAATAATCAACAATCTTAGAAGAGAAAAAATGATGATCCCATAGAACTAT 195
QY 123 TGCTCAGCTAAGGATCTGATGGCCAAAAGGAAGTGTGTTGTCGACGAAAGACATCTG 182
DB 194 TAAACAGTTAAGACCTTATGGAGAGAAAGAGATCTTTGTTGCATCCAAAAGCTACTG 135
QY 183 CCCTTACTGTAAAGCTACTTTGTCTACCTCTTCCAAAGATGAACGTTCCCAATCCAA 242
DB 134 CCCTACTGCGATGAGCTCTAAACAGCGCTTTTCGAGAGCTGAAGGTTCCAAAGTCCAA 75
QY 243 GGCCTTGTGTTGAATTAGATGAATGACCAATGGCTCAGAGATTCAAGACGCTTTAGA 302
DB 74 AGTTTGTGTTTCAATTAACGAGATGAAGGATGGCGCAGACATTCAGCGCGGTACA 15
QY 303 AGAAATCTCGGGC 316
DB 14 TGAGATTATGGCC 1

RESULT 9
T37408/c
LOCUS 420 bp mRNA linear EST 11-JAN-1995
DEFINITION EST02526 S. cerevisiae strain X2180-1A Saccharomyces cerevisiae
cDNA 3' end, mRNA sequence.
T37408
T37408.1 GI:621225
EST.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
1 (bases 1 to 420)
Weinstock, K.
Saccharomyces cerevisiae cDNAs
Unpublished (1995)
Contact: Weinstock, K. and Venter, J.C.
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability please contact the TIGR Database
(tdbinfo@db.tigr.org)
Seq primer: M13-21.
Location/Qualifiers
1. .420
/organism="Saccharomyces cerevisiae"
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/strain="X2180-1A"
/db_xref="taxon:4932"
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/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

FEATURES
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FEATURES
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/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

XhoI

ORIGIN
Query Match 21.8%; Score 94; DB 10; Length 420;
Best Local Similarity 61.0%; Pred. No. 1e-14;
Matches 183; Conservative 0; Mismatches 114; Indels 3; Gaps 2;
QY 135 GGATCTGATTGCCCAAGGAAGTGTGTTGTCAGCAAGACATCTG-CCCTTACTGTA 193
DB 420 GGACCCCTATTTCAGAAAACGAGATCCTCGTCGATCCAAACCGCTACTGCCCCATCTGCC 361
QY 194 AAGCTACTTTGTCTACCTCTTCCAAAGATGAACG--TTCCCAATCCAAGGCCCTTGT 251
DB 360 ATGCGCCCTTAAACACGCTTTTGAAGATTAAAGGTTCCCAAGTCCCAAGTCTCGT 301
QY 252 GTTGAATTAGATAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAGAAATCTC 311
DB 300 TTTCGNATTGAATGACATGAAGGAAGGCGCAGACATTCAGGCTGCGCTTATATGAGATTAA 241
QY 312 GGGCCAAAACCTGACCTAACGTATACATCAATGCGAAGCACATTTGGTGGTAACAGCGA 371
DB 240 TGGCCAAAAGACCGTCCCAACATCTATATTATGTTAAACATATTGGAAGGCAACGACCA 181
QY 372 TTTGGAACCTTTGAAGAAAAATGCAAGTTAGCTGAAATATTGAAGCCGCTATTTCATTA 431
DB 180 CTTGCGGGAATTGAGGAGACTGGTGAATTGAGGNATTGTTAGAACCTATTCTTTCGAAA 121

RESULT 10
AZ926128/c
LOCUS 454 bp DNA linear GSS 01-APR-2001
DEFINITION 476.dio41e06.sl Saccharomyces castellii NRRL Y-12630 Saccharomycetes
castellii genomic clone 476.dio41e06.sl, genomic survey sequence.
AZ926128
AZ926128.1 GI:13497029
GSS.
Saccharomyces castellii
Saccharomycetes castellii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
1 (bases 1 to 454)
Clifton, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T.,
Gish, W.R., Waterston, R.H. and Johnston, M.
Surveying Saccharomycetes genomes to identify functional elements by
comparative DNA sequence analysis
Unpublished (2001)
Contact: Johnston M
Department of Genetics
Washington University Medical School
Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
Tel: 314 362 2735
Fax: 314 362 7855
Email: mj@genetics.wustl.edu
Class: random plasmid subclone.
Location/Qualifiers
1. .454
/organism="Saccharomyces castellii"
/mol_type="genomic DNA"
/strain="NRRL Y-12630 (CBS 4309)"
/db_xref="taxon:27288"
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FEATURES
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Location/Qualifiers
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/note="Random genomic sequence"

FEATURES
source
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/note="Random genomic sequence"

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Best Local Similarity 66.8%; Pred. No. 8.9e-14;
Matches 129; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 239 CCAAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATCGCTCAGAGATTCAAGACGCTT 298
DB 454 CAAAGCCCTTAGTGTGTCATTAATGAATGAATGATGGTCTGCTGAATCCCAAGCCT 395

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Qy 299 TAGAAGAAATCTCGGCGCAAAAAAAGTGTACTTAACGATGATACATCAATGCGAAGCACATTG 358
Db 394 TATTGAAATTAATGGCCAAAGACCGTTCCAAATATTTACATCAATGGTAAGCACGTTG 335
Qy 359 GTGCTACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAATATTGAAGC 418
Db 334 GTGGGAACGATTAATTCAGACTTGAAGAAATCTGGTGAATTGGAAGATTTATTGGAGC 275
Qy 419 CGGTATTTCATA 431
Db 274 CAATCTGGAGTA 262

RESULT 11
LOCUS C2286838 848 bp DNA linear GSS 01-JUL-2005
DEFINITION cp49c01.r Candida parapsilosis Random Genomic Library Candida
parapsilosis genomic clone cp49c01, genomic survey sequence.
ACCESSION C2286838
VERSION C2286838.1 GI:68458148
KEYWORDS GSS.
SOURCE Candida parapsilosis
ORGANISM Candida parapsilosis
REFERENCE 1 (bases 1 to 848)
AUTHORS Logue, M.E., Wong, S., Wolfe, K.H. and Butler, G.
TITLE A genome sequence survey shows that the pathogenic yeast Candida
parapsilosis has a defective MTL1 allele at its mating type locus
JOURNAL Eukaryot. Cell 4 (6), 1009-1017 (2005)
PUBMED 15947193
COMMENT Contact: Logue M
Department of Biochemistry, Conway Institute of Biomolecular and
Biomedical Research
University College Dublin
Dublin 4, Ireland
Tel: +353 1 7166885
Fax: +353 1 2837211
Email: mary.e.logue@ucd.ie
Class: plasmid ends.
FEATURES
Location/Qualifiers
1..848
/organism="Candida parapsilosis"
/mol_type="genomic DNA"
/strain="CL18214"
/db_xref="taxon:5480"
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Query Match 16.8%; Score 72.4; DB 13; Length 848;
Best Local Similarity 59.1%; Pred. No. 1e-08;
Matches 149; Conservative 0; Mismatches 91; Indels 12; Gaps 1;
Qy 150 AAAGGAAGTGTGTTGTCAGCAAGACATCTGCCCTTACTGTAAAGCTACTTGTCTAC 209
Db 444 AAACAAGATCTAGTGTATTCAAAACCTACTGCCCTTATGTACCCGCCAAGGATTT 385
Qy 210 CCTCTTCCAAGATTGAACGTTCCCAATCAAGGCCCTTGTGTGGAATTAGATGAAT 269
Db 384 ACTAGGAAGATGTGGATCGATTACAAAT-----TGATTGAATTGAATACAC 337
Qy 270 GAGCAATGGCTCAGAGATTCAGACGCTTTAGAGAATAATCTCGGCCAAAACCTGTACC 329
Db 336 TTCAGATGGCGGTGAGGTTTCAGCGTGCACTACAGAATAATCAGCGGTCAAAGAACTGTACC 277
Qy 330 TAACGTATACATCAATGCAAGACATTTGGTGTAAACGCGATTGTGAAACTTTGAAGAA 389
Db 276 AAATGTTTTCATCAATGGTGAGCATATCGGAGGTAATCTGATTTGCAAGCCTTAGAGAG 217
Qy 390 AAATGGCAAGTT 401
Db 216 TAAAGGAGAGTT 205

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RESULT 12

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LOCUS DN156309 492 bp mRNA linear EST 18-FEB-2005
DEFINITION GCA001D02x GCA Hordeum vulgare cDNA clone GCA001D02 3-PRIME, mRNA
sequence.
ACCESSION DN156309
VERSION DN156309.1 GI:59942203
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
REFERENCE 1 (bases 1 to 492)
AUTHORS Biemelt, S., Jansen, C., Schaefer, P., Hueckelhoven, R., Felk, A.,
Schaefer, W., Scholz, U., Sonnwald, U., and Kogel, K.H.
TITLE Barley ESTs from different tissues challenged with fungal pathogens
JOURNAL Unpublished (2004)
COMMENT Contact: Sophia Biemelt
Molecular Developmental Physiology, Department Molecular Cell
Biology
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466 Gatersleben, Germany
Tel: +49 (0)39482-5476
Fax: +49 (0)39482-5515
Email: biemelt@ipk-gatersleben.de
Insert length: 492 Std Error: 0.00
Plate: 1 row: D column: 2
Seq primer: pTriplex2.
FEATURES
Location/Qualifiers
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/organism="Hordeum vulgare"
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/cultivar="Chevron"
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/clone="GCA001D02"
/tissue_type="with Fusarium graminearum infected
spikelets"
/lab_host="E. coli BM25.8"
/clone_lib="GCA"
/notes="Vector: pTriplex2 (BD Biosciences); Site 1: Sf1a
(GGCCATTATGCC); Site 2: Sf1B (GGCCGCTCGGCC); Each second
spikelet of barley was infected with Fusarium graminearum
(strain FG2311, isolated from wheat, 1992, Hohenheim,
Germany) by means of micropipette using 5 microliter of
conidia suspension (500 conidia /microliter). The infected
plants were incubated 4d by 16 h light and 20 degree
celcius and infected spikes were incubated the first 48 h
by 100 % rel. humidity for establishing of infection.
PolyA-RNA was isolated from infected spikes and used to
create a cDNA-library using the Creator Lambda Triplex2
libraries kit (BD Biosciences). cDNA Fragments were
inserted into the vector pLambda-Triplex2. Subsequently,
plasmids were obtained by in vivo excision according to
manufacturers instruction. (GABI-Agrotech project)"
ORIGIN
Query Match 15.9%; Score 68.8; DB 9; Length 492;
Best Local Similarity 54.6%; Pred. No. 9e-08;
Matches 167; Conservative 0; Mismatches 127; Indels 12; Gaps 1;
Qy 116 AAACAGTGTCTACGTAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCGACGAAGA 175
Db 32 AAGCATCTACCAAGGTTACAGAGCTTATCGACAACAACCTGTGTGTCTCTCCAAAGT 91
Qy 176 CATACTGCCCTTACTGTAAGCTACTTTGTCTACCTCTTCCAAAGTAATGAAGCTCCCA 235
Db 92 CTTACTGCCCTTACTGCAAGACGACCAAGAAGATC-----TGGATGATTGA 139
Qy 236 AATCCAAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACG 295

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Db      140  ACACGAGTACGAGCTCTTGAGCTCGACGAAGTTTCCGATGGCTGCTCTCCAGGACG 199
Qy      296  CTTTAGAAGAAATCTCGGGCCAAAATACTGACTACCTACGCTATACATCAATGCGAAGCACA 355
Db      200  CTCTCGAAGAAGATCTCTGGCCAGCGTACCGTCCCAACGCTCTACATCAAGCAGCAGCACA 259
Qy      356  TTGGTGGTACAGCGATTTCGGAACCTTTGAAGAAAATGCAAGTTAGCTGAATATTGA 415
Db      260  TTGGTGGTAACTCAGACCTCAGAGCCTGAACCTCTGGCGGAAAGCTCAAGAACCTTCTCA 319
Qy      416  AGCCGG 421
Db      320  AGGAGG 325

RESULT 13
CN813116/c
LOCUS
DEFINITION
Fg06_03g17_R Fg06_AAPC_ECORC_Fusarium_graminearum_perithecia
CN813116
CN813116.1 GI:47837127
EST.
SOURCE
Gibberella zeae (anamorph: Fusarium graminearum)
ORGANISM
Gibberella zeae
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
1 (bases 1 to 529)
Harris,L.J., Rocheleau,H., Ouellet,T., Allard,S., Chapados,J.,
Couroux,P., De Moors,A., Hattori,J.I., Lacroix,C., Masotti,M.,
Robert,L.S., Singh,J.A., Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Fusarium graminearum enriched for late
stage perithecia
Unpublished (2004)
JOURNAL
Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrislj@agr.gc.ca.
FEATURES
Source
1. 529
/organism="Gibberella zeae"
/mol_type="mRNA"
/strain="DAOM 180378"
/db_xref="taxon:5518"
/clone="Fg06_03g17"
/lab_host="E. coli DH10B"
/clone_lib="Fg06_AAPC_ECORC_Fusarium_graminearum_perithecia"
a"
/note="Vector: pGem-T easy; Site 1: EcoRI; Mycelia grown
on carrot agar at 200C until confluent; perithecia induced
with Tween 40 solution (25% v/v). Fruiting bodies were
collected 20 days after induction. Total RNA was extracted
using Trizol. cDNAs were amplified using Invitrogen
GeneRacer kit. cDNA was not fractionated and was
bidirectionally cloned."
ORIGIN
Query Match 15.8%; Score 68.4; DB 8; Length 529;
Best Local Similarity 54.2%; Pred. No. 1.2e-07;
Matches 166; Conservative 1; Mismatches 127; Indels 12; Gaps 1;
Qy 116 AACAGTTGCTCAGTAAAGATCTGATGGCCAAAAGGAGTGTGTTGTCAGCAAGA 175
Db 491 AAGCATCTACCAAGGTTTCAGCAGCTTATCGACAACAACCTCTGTTGTTCTCTCAAGT 432
Qy 176 CATACTGCCCTTACTGTAAGCTACTTTGTCTACCTCTTCCAGAATTGAACGTTCCCA 235

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Db      431  CTTACTGCCCTTACTGCAAGCAGACCAAGAAGACTC-----TGATGATTGTA 384
Qy      236  AATCCAAGGCCCTTGTGTTGGAAATTAGATGAATGAGCAATGGCTCAGAGATTCAGACG 295
Db      383  ACACCGAGTACGAGCTCTTGGAGCTCGACGAAGTTTCCGATGGCTGCTCTCCAGGACG 324
Qy      296  CTTTAGAAGAAATCTCGGGCCAAAATACTGACTACCTACGCTATACATCAATGCGAAGCACA 355
Db      323  CTCTCGAAGAAGATSTCTGGCCAGCGTACCGTCCCAACGCTCTACATCAAGCAGCAGCACA 264
Qy      356  TTGGTGGTAACTCAGACCTTCCAGAGCCTGAACCTCTGGCGGAAAGCTCAAGAACCTTCTCA 415
Db      263  TTGGTGGTAACTCAGACCTTCCAGAGCCTGAACCTCTGGCGGAAAGCTCAAGAACCTTCTCA 204
Qy      416  AGCCGG 421
Db      203  AGGAGG 198

RESULT 14
CN813786
LOCUS
DEFINITION
Fg06_04h05_R Fg06_AAPC_ECORC_Fusarium_graminearum_perithecia
CN813786
CN813786.1 GI:47837797
EST.
SOURCE
Gibberella zeae (anamorph: Fusarium graminearum)
ORGANISM
Gibberella zeae
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
1 (bases 1 to 522)
Harris,L.J., Rocheleau,H., Ouellet,T., Allard,S., Chapados,J.,
Couroux,P., De Moors,A., Hattori,J.I., Lacroix,C., Masotti,M.,
Robert,L.S., Singh,J.A., Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Fusarium graminearum enriched for late
stage perithecia
Unpublished (2004)
JOURNAL
Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrislj@agr.gc.ca.
FEATURES
Source
1. 522
/organism="Gibberella zeae"
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/strain="DAOM 180378"
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/clone="Fg06_04h05"
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/lab_host="E. coli DH10B"
/clone_lib="Fg06_AAPC_ECORC_Fusarium_graminearum_perithecia"
a"
/note="Vector: pGem-T easy; Site 1: EcoRI; Mycelia grown
on carrot agar at 200C until confluent; perithecia induced
with Tween 40 solution (25% v/v). Fruiting bodies were
collected 20 days after induction. Total RNA was extracted
using Trizol. cDNAs were amplified using Invitrogen
GeneRacer kit. cDNA was not fractionated and was
bidirectionally cloned."
ORIGIN
Query Match 15.7%; Score 68; DB 8; Length 522;
Best Local Similarity 52.9%; Pred. No. 1.5e-07;
Matches 162; Conservative 6; Mismatches 126; Indels 12; Gaps 1;
Qy 116 AACAGTTGCTCAGTAAAGATCTGATGGCCAAAAGGAGTGTGTTGTCAGCAAGA 175
Db 32 AAGCATCTACCAAGGTTTCAGCAGCTTATCGACAACAACCTCTGTTGTTCTCTCAAGT 91

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QY 176 CATACTGCCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAGAATTGAAGCTTCCCA 235
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Db 92 CTTACTSCCCTACTGCAAGCAGACCAAGAAGCTC-----TGGATGATTGA 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 236 AATCCAAAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACG 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 140 ACACCGAGTACGAGCTCTTTGAGCTCGACGAAGTTTCCGATGGCTCTGTCTCTCCAGGACG 199
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QY 296 CTTTGAAGAAATCTCGGGCCAAAAAATCTACTACGTATACATCATCAATGGCAAGCACA 355
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Db 200 CTCTCGAAGATCTCTGGCCAGGTTACCGYCCCAACGTTCTACATCAGCAGCAGCACA 259
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QY 356 TTGGTGTAAACAGCGATTTTGGAAATTTTGAAGAAAAATGCAAGTTAGCTGAAATATTGA 415
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Db 260 TTGGTGTAACTCAGACCTCCAGACCTGAACTCTGGCGAAAGCTCAAGAMCTTCTCA 319
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QY 416 AGCCGG 421
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Db 320 AGGAGG 325

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RESULT 15
CD459632/c
LOCUS
DEFINITION
  CD459632 477 bp mRNA linear EST 14-JUN-2004
  Fg09_06j07 A Fg09 AAPC ECORC Fusarium graminearum simple_substrate
  Gibberella zeae cDNA clone Fg09_06j07, mRNA sequence.
ACCESSION
  CD459632
KEYWORDS
  CD459632.2 GI:48689774
SOURCE
  EST.
ORGANISM
  Gibberella zeae (anamorph: Fusarium graminearum)
  Gibberella zeae
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
  Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
  1 (bases 1 to 477)
  Watson, R.J., Heyls, R., Couroux, P., De Moors, A., Harris, L.J.,
  Hattori, J., Lacroix, C., Masotti, M., Ouellet, T., Robert, L.S.,
  Singh, J.A., Sprott, D. and Tinker, N.A.
  A cDNA library prepared from Fusarium graminearum grown on a simple
  substrate
  Unpublished (2003)
  On Jun 3, 2003 this sequence version replaced gi:31374372.
  Contact: Watson, Robert.J.
  Eastern Cereal and Oilseed Research Centre
  Agriculture and Agri-food Canada
  Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
  CANADA
  Tel: (613) 759-1655
  Fax: (613) 759-1701
  Email: watsonrj@agr.gc.ca.
  Location/Qualifiers
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      /organism="Gibberella zeae"
      /mol_type="mRNA"
      /strain="DAOM 180378"
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      /notes="Vector: pBluescript II+; Site 1: EcoRI; Site 2:
      XhoI; Fusarium graminearum grown on a simple substrate--
      minimal media supplemented with amino acids."

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FEATURES

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    /mol_type="mRNA"
    /strain="DAOM 180378"
    /db_xref="taxon:5518"
    /clone="Fg09_06j07"
    /tissue_type="Mycelium"
    /dev_stage="Asexual"
    /lab_host="E. coli DH10B"
    /clone_lib="Fg09_AAPC_ECORC_Fusarium_graminearum_simple_su
    bstrate"
    /notes="Vector: pBluescript II+; Site 1: EcoRI; Site 2:
    XhoI; Fusarium graminearum grown on a simple substrate--
    minimal media supplemented with amino acids."

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ORIGIN

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Query Match      15.6%; Score 67.6; DB 5; Length 477;
Best Local Similarity 55.2%; Pred. No. 1.9e-07;
Matches 158; Conservative 1; Mismatches 115; Indels 12; Gaps 1;
QY 116 AAACAGTTGCTCAGTAAAGATCTGATTGCCAAAAGGAAGTGTTTGTTGCAGCAAGA 175
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Db 448 AAGCATCTACCAAGGTTTCAGCAGCTTATCGAACAACTCTGTGTGTTCTTCTCCAAGT 389
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QY 176 CATACTGCCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAGAATTGAAGCTTCCCA 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 CTTACTGCCCTACTGCAAGCAGACCAAGAAGCTC-----TGGATGATTGA 341
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QY 236 AATCCAAAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACG 295
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Db 340 ACACCGAGTACGAGCTCTTTGAGCTCGACGAAGTTTCCGATGGCTCTGTCTCTCCAGGACG 281
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Db 280 CTCTCGAAGATCTCTGGCCAGGTTACCGTCCCAACGTTCTACATCAGCAGCAGCACA 221
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Db 220 TTGGTGTAACTCAGACCTCCAGACCTGAACTCTGGCGAAAGCTCAAGAMCTTCTCA 175
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-10-523-362-3
Perfect score: 432
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

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- 2: /EMC Celerra_SIDS3/ptodata/2/ina/5 COMB.seq.*
- 3: /EMC Celerra_SIDS3/ptodata/2/ina/6A COMB.seq.*
- 4: /EMC Celerra_SIDS3/ptodata/2/ina/6B COMB.seq.*
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- 8: /EMC Celerra_SIDS3/ptodata/2/ina/RE COMB.seq.*
- 9: /EMC Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq.*
- 10: /EMC Celerra_SIDS3/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	75.2	17.4	183	3	US-09-248-796A-4011
2	69.8	16.2	582	3	US-09-248-796A-4012
3	64.6	15.0	681	3	US-08-998-416-1146
4	45.6	10.6	453	3	US-09-270-767-758
5	45.6	10.6	453	3	US-09-270-767-16040
6	44	10.2	302	3	US-09-313-294A-4085
7	43.2	10.0	497	3	US-09-621-976-1270
8	43.2	10.0	654	2	US-08-911-319A-2
9	43.2	10.0	654	3	US-09-352-619-2
10	42	9.7	2191	3	US-09-127-219B-1
11	39	9.0	522	3	US-09-162-564-1
12	38.8	9.0	474	3	US-09-621-976-1272
13	37.4	8.7	519	3	US-09-513-999C-3976
14	36.4	8.4	530	3	US-09-621-976-1271
15	36.2	8.4	837	4	US-09-880-107-3793
16	34.8	8.1	580073	3	US-08-545-528B-1
17	34.6	8.0	1830121	3	US-09-557-884-1
18	34.6	8.0	1830121	3	US-09-643-990A-1
19	34.6	8.0	1830121	3	US-10-158-865-1
20	34.4	8.0	603	3	US-09-533-559-3294
21	34.4	8.0	3258	3	US-09-328-352-587
22	34.4	8.0	9408	3	US-09-418-710-14
23	34.4	8.0	9408	3	US-09-839-479-14

24	34.2	7.9	479	3	US-08-899-786-17	Sequence 17, Appl
25	34.2	7.9	1103	3	US-08-899-786-13	Sequence 13, Appl
26	34	7.9	77586	3	US-09-949-016-13220	Sequence 13220, A
27	34	7.9	77586	3	US-09-949-016-13221	Sequence 13221, A
C 28	33.6	7.8	474	3	US-09-621-976-18033	Sequence 18033, A
C 29	33.6	7.8	601	3	US-09-949-016-132474	Sequence 132474, A
C 30	33.6	7.8	601	3	US-09-949-016-173301	Sequence 173301, A
C 31	33.6	7.8	601	3	US-09-949-016-173302	Sequence 173302, A
C 32	33.6	7.8	141248	3	US-09-949-016-12241	Sequence 12241, A
C 33	33.6	7.8	143248	3	US-09-949-016-16652	Sequence 16652, A
C 34	33.6	7.8	450395	3	US-09-949-016-15473	Sequence 15473, A
C 35	33.6	7.8	451924	3	US-09-949-016-12896	Sequence 12896, A
C 36	33.6	7.8	451925	3	US-09-949-016-17305	Sequence 17305, A
C 37	33.6	7.8	636591	3	US-09-949-016-11808	Sequence 11808, A
C 38	33.6	7.8	636591	3	US-09-949-016-13388	Sequence 13388, A
C 39	33.2	7.7	468	3	US-09-134-000C-1668	Sequence 1668, Ap
40	33.2	7.7	484	3	US-08-899-786-18	Sequence 18, Appl
41	33.2	7.7	549	3	US-09-328-352-3243	Sequence 3243, Ap
C 42	33.2	7.7	601	3	US-09-949-002-7829	Sequence 7829, Ap
C 43	33.2	7.7	267482	3	US-09-949-002-659	Sequence 659, App
C 44	33.2	7.7	267505	3	US-09-949-002-783	Sequence 783, App
45	33	7.6	291	3	US-09-543-681A-1044	Sequence 1044, Ap

ALIGNMENTS

RESULT 1

US-09-248-796A-4011
; Sequence 4011, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 4011
; LENGTH: 183
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-4011

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Best Local Similarity	65.5%	Pred. No. 5.5e-13;		
Mismatches	110;	Conservative	0;	Mismatches 58; Indels 0; Gaps 0;
QY	254	TGGAATTAGATGAAATGACCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCGG	313	
Db	11	TTGAATTAGCAAGATTGACGCGGTGTAATCCAGAGCATTTATGGAATCACTG	70	
QY	314	GCACAAAACCTGACTTAACGTATACATCAATGGCAGCAGCATTTGGTGAACAGGATT	373	
Db	71	GTCAAGAAACCGTTCACAAATGCTTTATTGGTGTCAACATATTGGTGGCAATTCGATG	130	
QY	374	TGGAACCTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTGAAGCCGG	421	
Db	131	TGCAGCTTTGAATTTCTATTGACATTTAATAACAATTCACACCTG	178	

RESULT 2

US-09-248-796A-4012
; Sequence 4012, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

; Sequence 16040, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16040
; LENGTH: 453
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-16040

Query Match 10.6%; Score 45.6; DB 3; Length 453;
Best Local Similarity 54.9%; Pred. No. 0.00072;
Matches 90; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 234 CAAATCCAAGGCCCTTGTTGGAAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGA 293
DB 256 CAAGCTCAGGCAACGGTGATCGAGCTGGACCAGCGGATGATGCAACGAGATCCAGGC 315
QY 294 CGCTTTAGAGAAATCTCGGSCCAAAAACCTGTACCTAACTATACATATACATCAATGCAAGCA 353
DB 316 GGTCTTGGCGAGATGACGGCTCGAGACCGTTCCACGTTGCTTCATCGATGCAAGTT 375
QY 354 CATTGCTGTACAGCATTTGGAACCTTTGAAGAAAATGGCA 397
DB 376 CGTGGTGGCGGCCCGACGCTGAAGCGCTATACGACAGGGCA 419

RESULT 6

US-09-313-294A-4085
; Sequence 4085, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4085
; LENGTH: 302
; TYPE: DNA
; ORGANISM: *Zea mays*
; FEATURES:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6476212 700347664H1
; NAME/KEY: unsure
; LOCATION: 2, 27, 106, 120, 130, 162, 189, 287
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4085

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Best Local Similarity 62.4%; Pred. No. 0.0018;
Matches 68; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 254 TGAATTAGAATGAGCAATGGCTCAGAGATTCAAGAGCTTTAGAGAAATCTCGG 313
DB 174 TTGAGTTGGATGAGNCAGTGTGAGCTGAGCTCCAGAAATGCCCTGAAGGAGTGGACTG 233
QY 314 GCCAAAACCTGTACCTAACTATACATCAATGCGCAAGCATTGGTGG 362
DB 234 GACAGAGACTGTCCCAAAATGCTTCATCAATGGGAAGCATATTTGGCGG 282

RESULT 7

US-09-621-976-1270
; Sequence 1270, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1270
; LENGTH: 497
; TYPE: DNA
; ORGANISM: *Homo sapiens*
; FEATURES:
; NAME/KEY: CDS
; LOCATION: 154..495
US-09-621-976-1270

Query Match 10.0%; Score 43.2; DB 3; Length 497;
Best Local Similarity 55.3%; Pred. No. 0.004;
Matches 84; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 250 GTGTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATC 309
DB 319 GTGTGGAATGACCTGCTTGAATATGGAACAGTTCAGAGATGCTCTTTACAAATG 378
QY 310 TCGGGCCAAAACCTGTACCTAACGTATACATCAATGGCAAGCAGCATTTGGTGAACAGC 369
DB 379 ACTGGTGGAAGAACTGTTCCAGAAATATTTGTCAATGTAATTTTATTTGGAGGTGCAACT 438
QY 370 GATTGGAACCTTTGAAGAAAATGCAAGTT 401
DB 439 GACACTCATAGGCTTCACAAAGGAAGAAAT 470

RESULT 8

US-08-911-319A-2
; Sequence 2, Application US/08911319A
; Patent No. 5968798
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,319A
; FILING DATE: August 14, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Muenzen, Colette C.
; REGISTRATION NUMBER: 39,784
; REFERENCE/DOCKET NUMBER: PF-0363 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555

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TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 654 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPINOT03
; CLONE: 2447829
US-08-911-319A-2

Query Match 10.0%; Score 43.2; DB 2; Length 654;
Best Local Similarity 55.3%; Pred. No. 0.0045;
Matches 84; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 250 GTGTTGGAATTAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAGAAATC 309
DB 296 GTGGTGGAACTGGACCTGCTTGAATATGAAACCAAGTTCGAAGATGCTTTTACAAAATG 355
QY 310 TCGGGCCAAAAAAGTGTACCTAACGTATACATCAATGCGCAAGCACATTTGGTGGTAAACAGC 369
DB 356 ACTGGTGAAGAACTGTTCCAGAAATATTGTCAATGGTACTTTTATTGGAGGTGCAACT 415
QY 370 GATTGGAACTTTGAAGAAAAATGCGAAGTT 401
DB 416 GACACTCATAGGCTTCACAAAGAGAGAAAAATT 447

RESULT 9
US-09-352-619-2
; Sequence 2, Application US/09352619
; Patent No. 6084070
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/352,619
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,319
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Muenzen, Colette C.
; REGISTRATION NUMBER: 39,784
; REFERENCE/DOCKET NUMBER: PF-0363 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 654 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPINOT03
; CLONE: 2447829

TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 654 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPINOT03
; CLONE: 2447829
US-08-911-319A-2

Query Match 10.0%; Score 43.2; DB 2; Length 654;
Best Local Similarity 55.3%; Pred. No. 0.0045;
Matches 84; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 250 GTGTTGGAATTAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAGAAATC 309
DB 296 GTGGTGGAACTGGACCTGCTTGAATATGAAACCAAGTTCGAAGATGCTTTTACAAAATG 355
QY 310 TCGGGCCAAAAAAGTGTACCTAACGTATACATCAATGCGCAAGCACATTTGGTGGTAAACAGC 369
DB 356 ACTGGTGAAGAACTGTTCCAGAAATATTGTCAATGGTACTTTTATTGGAGGTGCAACT 415
QY 370 GATTGGAACTTTGAAGAAAAATGCGAAGTT 401
DB 416 GACACTCATAGGCTTCACAAAGAGAGAAAAATT 447

RESULT 10
US-09-127-219B-1
; Sequence 1, Application US/09127219B
; Patent No. 6372772
; GENERAL INFORMATION:
; APPLICANT: KIRKPATRICK, D. LYNN
; APPLICANT: POWIS, GARTH
; TITLE OF INVENTION: INHIBITORS OF REDOX SIGNALING AND METHODS OF USING SAME
; FILE REFERENCE: 98-571-us
; CURRENT APPLICATION NUMBER: US/09/127,219B
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/054,566
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-127-219B-1

Query Match 9.7%; Score 42; DB 3; Length 2191;
Best Local Similarity 60.5%; Pred. No. 0.017;
Matches 69; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 249 TGTGTGGAATTAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAGAAAT 308
DB 94 TGTCTTGGAACTTGATCAAGTTGATGATGGGGCCAGGGTTCAAGAAAGTCTGTCTCAGAAAT 153
QY 309 CTCGGGCCAAAAAAGTGTACCTAACGTATACATCAATGCGCAAGCACATTTGGTGG 362
DB 154 CACTAATCAGAAAACTGTGCCCAATATTTCGTGAATAAAGTGCATGTAGGTGG 207

RESULT 11
US-09-162-564-1
; Sequence 1, Application US/09162564
; Patent No. 6379664
; GENERAL INFORMATION:
; APPLICANT: Lou, Marjorie
; APPLICANT: Raghavachari, Nalini
; APPLICANT: Qiao, Fengyu
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR THE PREVENTION AND TREATMENT
; FILE REFERENCE: UNL-98-2-1
; CURRENT APPLICATION NUMBER: US/09/162,564
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (4)...(324)
US-09-162-564-1

Query Match      9.0%; Score 39; DB 3; Length 522;
Best Local Similarity 58.0%; Pred. No. 0.076;
Matches 69; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 283 GAGATTCAAGACGCTTTAGAGAAATCTCGGGCCCAAAAAAAGTGTACCTAAACGTATACATC 342
Db 169 GAGATTCAAGATTATCTGCAACAGCTCACAGGAGCCAGACGGTACCTCGGTCCTTTATC 228

Qy 343 AATGGCAAGCACATTTGGTGTAAACAGGATTTGAAACTTTGAAGAAAAATGGCAAGTT 401
Db 229 GGTAAGAGTGTATAGTGGATGATCTAGTAAGATGATGCAACAGAGAGGGAGCT 287

RESULT 12
US-09-621-976-1272
; Sequence 1272, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1272
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 193..474
US-09-621-976-1272

Query Match      9.0%; Score 38.8; DB 3; Length 474;
Best Local Similarity 58.8%; Pred. No. 0.083;
Matches 67; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 250 GTGTTGGAATTAGATGAATGAGCAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATC 309
Db 358 GTGTTGGAATCGGACCTGCTTGAATATGGAACCAAGTCCAAAGATGCTCTTTACAAATG 417

Qy 310 TCGGGCCCAAAAAAAGTGTACCTAACTATACATCAATGGCAAGCACATTTGGTGGT 363
Db 418 ACTGTGAAGAACTGTTCCAAGATATTTGTCAATGGTACTTTTATTTGGAGGT 471

RESULT 13
US-09-513-999C-3976
; Sequence 3976, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT NO. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3976
; LENGTH: 519
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 116..433
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 340
; OTHER INFORMATION: y=c or t
US-09-513-999C-3976

Query Match      8.7%; Score 37.4; DB 3; Length 519;
Best Local Similarity 57.5%; Pred. No. 0.23;
Matches 65; Conservative 1; Mismatches 47; Indels 0; Gaps 0;

Qy 283 GAGATTCAAGACGCTTTAGAGAAATCTCGGGCCCAAAAAAAGTGTACCTAAACGTATACATC 342
Db 281 GAGATTCAAGATTATTTTGCACAGCTCACGGGAGCAAGAACGGTGCCTCGAGTCTTTATY 340

Qy 343 AATGGCAAGCACATTTGGTGTAAACAGGATTTGGAACCTTTGAAGAAAAATGG 395
Db 341 GGTAAAGATTGTATAGCGGATGCGAGTATAGTCTCTTTGCAACAGAGTGG 393

RESULT 14
US-09-621-976-1271
; Sequence 1271, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1271
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 378..530
US-09-621-976-1271

Query Match      8.4%; Score 36.4; DB 3; Length 530;
Best Local Similarity 58.2%; Pred. No. 0.46;
Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 250 GTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATC 309
Db 420 GTGTTGGAATCGGACCTGCTTGAATATGGAACCAAGTTCCAAGATGCTCTTTACAAATG 479

Qy 310 TCGGGCCCAAAAAAAGTGTACCTAACTATACATCAATGGCAAGCACATTTGG 359
Db 480 ACTGTGAAGAACTGTTCCAAGATATTTGTCAATGGTACTTTTATTTGG 529

RESULT 15
US-09-880-107-3793
; Sequence 3793, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2006, 03:35:08 ; Search time 1459 Seconds
(without alignments)
3638.285 Million cell updates/sec

Title: US-10-523-362-3

Perfect score: 432

Sequence: 1 atggagacaaatttcttctt.....tgaagccggtatttcaatag 432

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:*

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- 2: /EMC_Celerra_SID33/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SID33/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
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- 9: /EMC_Celerra_SID33/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SID33/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SID33/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SID33/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SID33/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SID33/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SID33/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SID33/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	432	100.0	432	11	US-10-932-182A-76174
2	432	100.0	432	12	US-10-523-362-3
3	432	100.0	932	8	US-10-451-467A-133
4	336.6	77.9	570	11	US-10-932-182A-3898
5	153.8	35.6	345	11	US-10-932-182A-3588
6	147.4	34.1	833	8	US-10-451-467A-65
7	146.6	33.9	333	11	US-10-932-182A-75707
8	143.4	33.2	333	12	US-10-523-362-1
9	89	20.6	360	7	US-10-032-585-6780
10	89	20.6	360	8	US-10-451-467A-607
11	61	14.1	609	9	US-10-425-115-146552
12	56	13.0	377	9	US-10-425-115-149360
13	56	13.0	578	16	US-11-096-568A-26783
14	55.6	12.9	721	8	US-10-437-963-29343
15	55.6	12.9	733	12	US-10-523-362-47
16	55	12.7	278	3	US-09-923-876-5514
17	55	12.7	278	3	US-09-923-876-5514

18	55	12.7	628	12	US-10-523-362-45	Sequence 45, Appl
19	55	12.7	763	9	US-10-425-115-44746	Sequence 44746, A
20	55	12.7	788	8	US-10-437-963-47111	Sequence 47111, A
21	55	12.7	877	9	US-10-425-115-44748	Sequence 44748, A
22	54.8	12.7	336	12	US-10-523-362-25	Sequence 25, Appl
23	53.2	12.3	649	9	US-10-425-115-177299	Sequence 177299, A
24	53.2	12.3	657	12	US-10-523-362-15	Sequence 15, Appl
25	50.2	11.6	628	8	US-10-767-701-11104	Sequence 11104, A
26	50	11.6	540	12	US-10-523-362-33	Sequence 33, Appl
27	49.2	11.4	449	3	US-09-535-459-73	Sequence 73, Appl
28	49.2	11.4	586	8	US-10-767-701-11645	Sequence 11645, A
29	49.2	11.4	597	9	US-10-425-115-127828	Sequence 127828, A
30	49.2	11.4	621	8	US-10-425-114-16796	Sequence 16796, A
31	49.2	11.4	864	8	US-10-425-114-25338	Sequence 25338, A
32	49.2	11.4	1579	9	US-10-425-115-127829	Sequence 127829, A
33	47.2	10.9	779	8	US-10-437-963-52359	Sequence 52359, A
C	34	47	282	11	US-10-932-182A-79774	Sequence 79774, A
35	46.8	10.8	385	3	US-09-732-627A-1485	Sequence 1485, Ap
36	46.8	10.8	590	8	US-10-021-323-8409	Sequence 8409, Ap
37	46.4	10.7	529	3	US-09-732-627A-628	Sequence 628, App
38	46.2	10.7	463	8	US-10-767-701-20293	Sequence 20293, A
39	46	10.6	481	9	US-10-425-115-123588	Sequence 123588, A
40	45.6	10.6	446	13	US-11-097-143-17639	Sequence 17639, A
41	45.6	10.6	478	13	US-11-097-143-15011	Sequence 15011, A
42	45.6	10.6	805	9	US-10-425-115-62369	Sequence 62369, A
43	45.6	10.6	1590	9	US-10-425-115-62371	Sequence 62371, A
44	45.6	10.6	2446	13	US-11-097-143-17638	Sequence 17638, A
45	45.4	10.5	672	12	US-10-523-362-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-10-932-182A-76174

; Sequence 76174, Application US/10932182A

; Publication No. US20060046253A1

; GENERAL INFORMATION:

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: 030685-043

; CURRENT APPLICATION NUMBER: US/10/932,182A

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: Patent in version 3.3

; SEQ ID NO 76174

; LENGTH: 432

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

US-10-932-182A-76174

Query Match	100.0%	Score 432;	DB 11;	Length 432;
Best Local Similarity	100.0%	Pred. No. 1.2e-111;		
Matches 432;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGGAGACCAATTTTTCCTCGACTCGAATTTAATTTGTTTATTATTCATTATCAGTTGTTT	60	
Db	1	ATGGAGACCAATTTTTCCTCGACTCGAATTTAATTTGTTTATTATTCATTATCAGTTGTTT	60	
Qy	61	GCACAGAAATTTTCTAAAGATTTTATCTACTCCAAAATGTTTCTCCAGGAACA	120	
Db	61	GCACAGAAATTTTCTAAAGATTTTATCTACTCCAAAATGTTTCTCCAGGAACA	120	
Qy	121	GTTCCTCAGTAAAGATCTGATTGCCAAAAGAAAGTGTTCCTGACGAAAGACATAC	180	
Db	121	GTTCCTCAGTAAAGATCTGATTGCCAAAAGAAAGTGTTCCTGACGAAAGACATAC	180	
Qy	181	TGCCCTTACTGTAAGCTACTTTTGTCTACCCCTCTTCAAGAAATGAACTGTTCCCAATCC	240	
Db	181	TGCCCTTACTGTAAGCTACTTTTGTCTACCCCTCTTCAAGAAATGAACTGTTCCCAATCC	240	

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Db 181 TGCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAGAATTGAACGTTCCCAATCC 240
Qy 241 AAGGCCCTTGTGTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
Db 241 AAGGCCCTTGTGTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
Qy 301 GAAGAAATCTCGGCCCAAAAACGTGTACCTAAAGTATACATCAATGGCAGCACATTGGT 360
Db 301 GAAGAAATCTCGGCCCAAAAACGTGTACCTAAAGTATACATCAATGGCAGCACATTGGT 360
Qy 361 GGTAAACAGCATTTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAATATTGAAGCCG 420
Db 361 GGTAAACAGCATTTGGAAACTTTGAAGAAAAATGGCAGTTAGCTGAAATATTGAAGCCG 420
Qy 421 GTATTTCATATAG 432
Db 421 GTATTTCATATAG 432

RESULT 2
US-10-523-362-3
; Sequence 3, Application US/10523362
; Publication No. US20060064784A1
; GENERAL INFORMATION:
; APPLICANT: Chardomans, Agnes
; APPLICANT: Puzio, Piotr
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Proteins Associated with Abiotic
; TITLE OF INVENTION: Stress Response
; FILE REFERENCE: 532622010300
; CURRENT APPLICATION NUMBER: US/10/523,362
; CURRENT FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(432)
; OTHER INFORMATION:
US-10-523-362-3

Query Match 100.0%; Score 432; DB 12; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.2e-111;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGACCAATTTTTCCTTCGACTCGAATTTAAATTTGTTATTATCATCATCAGTTGTTT 60
Db 1 ATGGAGACCAATTTTTCCTTCGACTCGAATTTAAATTTGTTATTATCATCATCAGTTGTTT 60
Qy 61 GCCACAAGAAATTTATGCTAAAGATTTTATCTACTCCAAAAATGGTATCCCAAGGAAACA 120
Db 61 GCCACAAGAAATTTATGCTAAAGATTTTATCTACTCCAAAAATGGTATCCCAAGGAAACA 120
Qy 121 GTTGCTCAGCTAAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 180
Db 121 GTTGCTCAGCTAAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 180
Qy 181 TGCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAGAATTGAACGTTCCCAATCC 240
Db 181 TGCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAGAATTGAACGTTCCCAATCC 240
Qy 241 AAGGCCCTTGTGTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
Db 241 AAGGCCCTTGTGTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
Qy 301 GAAGAAATCTCGGCCCAAAAACGTGTACCTCTTCCAGAATTGAACGTTCCCAATCC 360
Db 301 GAAGAAATCTCGGCCCAAAAACGTGTACCTCTTCCAGAATTGAACGTTCCCAATCC 360
Qy 361 GGTAAACAGCATTTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAATATTGAAGCCG 420
Db 361 GGTAAACAGCATTTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAATATTGAAGCCG 420
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Db 361 GGTAAACAGCATTTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAATATTGAAGCCG 420
Qy 421 GTATTTCATATAG 432
Db 421 GTATTTCATATAG 432

RESULT 3
US-10-451-467A-133
; Sequence 133, Application US/10451467A
; Publication No. US20040161840A1
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REEKMAN, RIEKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; TITLE OF INVENTION: YEAST AND FUNGI
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451,467A
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870003.9
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 732
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 133
; LENGTH: 932
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-133

Query Match 100.0%; Score 432; DB 8; Length 932;
Best Local Similarity 100.0%; Pred. No. 1.8e-111;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGACCAATTTTTCCTTCGACTCGAATTTAAATTTGTTATTATCATCATCAGTTGTTT 60
Db 501 ATGGAGACCAATTTTTCCTTCGACTCGAATTTAAATTTGTTATTATCATCATCAGTTGTTT 560
Qy 61 GCCACAAGAAATTTATGCTAAAGATTTTATCTACTCCAAAAATGGTATCCCAAGGAAACA 120
Db 561 GCCACAAGAAATTTATGCTAAAGATTTTATCTACTCCAAAAATGGTATCCCAAGGAAACA 620
Qy 121 GTTGCTCAGCTAAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 180
Db 621 GTTGCTCAGCTAAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 680
Qy 181 TGCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAGAATTGAACGTTCCCAATCC 240
Db 681 TGCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAGAATTGAACGTTCCCAATCC 740
Qy 241 AAGGCCCTTGTGTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
Db 741 AAGGCCCTTGTGTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 800
Qy 301 GAAGAAATCTCGGCCCAAAAACGTGTACCTTAACGTATACATCAATGGCAGCACATTGGT 360
Db 801 GAAGAAATCTCGGCCCAAAAACGTGTACCTTAACGTATACATCAATGGCAGCACATTGGT 860
Qy 361 GGTAAACAGCATTTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAATATTGAAGCCG 420
Db 861 GGTAAACAGCATTTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAATATTGAAGCCG 920
Qy 421 GTATTTCATATAG 432
Db 921 GTATTTCATATAG 932

RESULT 4
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US-10-932-182A-3898
; Sequence 3898, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3898
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-3898

Query Match 77.9%; Score 336.6; DB 11; Length 570;
Best Local Similarity 86.3%; Pred. No. 1.5e-84;
Matches 372; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

Qy 1 ATCGAGACCAATTTTCTTCGACTCGAATTTAATTTGTTATTTATCATTTATCACTGTTGTTT 60
Db 139 ATGGAACATAATTTTCTTCGACTCAAAATTTAATCGTTATTTGTTATTTATCATTTATCACTGTTGTTT 198
Qy 61 GCACAGAATTAATTTCTTAAGATTTTATCTACTCCAAATTTGTTATTTCCAGGAACA 120
Db 199 GCCACCAGATTTATCGCTAAGATTTTATCTACCCCAAAATTTGTTATTTCTCAAGAAACA 258
Qy 121 GTTGCTCAGTAAGATCTGATTGGCCAAAAGGAGTGTGTTGTCAGCAAGAGACATAC 180
Db 259 ATTGCACAGTAAGACCTTGATTGGCCAAAAGGAGTCTTCTGTTGCGGGAAGACATAC 318
Qy 181 TGGCCTTACTGTAAAGCTACTTTGTTACCTCTTTCCAAAGATTTGAAGCTTTCCCAATTC 240
Db 319 TGTCTTACTGTAAAGCCACATTTGTCACCTTTGTTCCAGGAATTTGAAGCTTTCCAAATTC 378
Qy 241 AAGGCCCTTGTGTGAATTAGAATGAGCAATGGCTCAGAGATTTCAAGACGCTTTA 300
Db 379 AAAGCCGTTGTTTGGAGTTGGACGAAATGAGCAATTTGTTCAAGAAATCCAGATGCTCTC 438
Qy 301 GAAGAAATCTCGGGCCAAAATACTGTACCTTAAGTATACATCAATGGCAAGCAGATCGT 360
Db 439 GAAGAAATTTTCGGCCAAAAGAACTGTACCAAAAGCTTTACATCAATGGTAAAGCAGATCGT 498
Qy 361 GGTAACAGCGATTGGAAATCTTTGAAGAAAATTTGCAAGATTTAGCTTGAATATTGAAGCCG 420
Db 499 GGAACAGCGATTGGAAAGCTTTGAAGAAAATTTGCAAGATTTAGCTTGAATATTGAAGCCG 558
Qy 421 GTATTTCAATA 431
Db 559 GTTTTCAATA 569

RESULT 5
US-10-932-182A-3588
; Sequence 3588, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3588
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-932-182A-3588

Query Match 34.1%; Score 147.4; DB 8; Length 833;
Best Local Similarity 65.2%; Pred. No. 7.3e-31;
Matches 217; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

Qy 99 AAAAAATGGTATCCAGGAAACAGTTGCTCACTAAAGATCTGATTGGCCAAAAAGGAAGT 158
Db 497 AAAAAATGGTATCTCAGAAACTATCAAGCAGCTCAAGGACCTTTATTCAGAAACGAGAT 556
Qy 159 GTTTGTTGCGCAAGAAACAGACTGCGCTTACTGTAAAGCTACTTTGTCTACCTCTTCCA 218

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Db 557 CTTGTCGCAATCCAAACGCTACTGTCCATCTGCCATGACGCCCTAAACACGCTTTTGA 616
QY 219 AGAATTGAACGTTCCCAATCCAAAGCCCTGTGTTGGAATTAGATGAATAGCAATGG 278
Db 617 AAAGTTAAAGGTTCCCAAGTCCAAAGTCTGTTGTTTTCGAATTGAATGACATGAAGGAGG 676
QY 279 CTGAGAGATTCAAGACGCTTTAGAAGAAATCTCGGGCCAAACAACTGTACCTAACGTATA 338
Db 677 CGCAGACATTTCAGGCTGCGTTATGAGATTAATGGCCAAAGAACCGTGCACAACTCTA 736
QY 339 CATCAATGGCAAGCACATTGCTGTAAACAGCGATTGGAACCTTTGAAGAAAAATGCAA 398
Db 737 TATTAATGGTAACATATTGGAGCGACGACGACTTTCGAGGAATGAGGAGACTGGTGA 796
QY 399 GTTAGCTGAATATTGAAGCCGCTATTTCATA 431
Db 797 ATTGGAGGAATTGTTAGAACCTATTCTTGCAA 829

RESULT 7

US-10-932-182A-75707
; Sequence 75707, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75707
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-75707

Query Match 33.9%; Score 146.6; DB 11; Length 333;
Best Local Similarity 65.3%; Pred. No. 7.8e-31;
Matches 215; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 103 ATGGTATCCCAGGAACAGTTGCTCAGTTAAAGGATCTGATTGGCCAAAGGAAGTGT 162
Db 1 ATGGTATCTCAAGAACTATCAAGCAGTCAAGGACCTTATTGCGAAGAACGAGATCTTC 60
QY 163 GTTGCAGCAAGACATACTGCCCTTACTGTAAAGCTACTTTGTCTACCCCTTTTCCAAGAA 222
Db 61 GTCGCATCCAAACGCTACTGTCATCTGCGATGCGCCCTAAACACGCTTTTGAAGAA 120
QY 223 TTGAAGCTTCCCAATCCAAAGCCCTGTGTTGGAATTAGATGAATGACATGCGCTCA 282
Db 121 TTAAGGTTCCCAAGTCCAAAGTCTGTTTTCGAATTGAATGACATGAAGGAAGCGCA 180
QY 283 GAGATTCAAGACGCTTTAGAAGAAATCTCGGGCCAAACAACTGTACTAACGTATACATC 342
Db 181 GACATTCAGGCTGGTTTATATGAGATTAAATGGCCAAAGAACCGTGCACAAACATCTATAT 240
QY 343 AATGGCAAGCACATTTGGTGGTAAACAGCGATTGGAACCTTTGAAGAAAAATGCGCAAGTTA 402
Db 241 AATGGTAAACATATTGAGGCAACGACGATTTCGAGGAATTGAGGAGACTGCGCAATTG 300
QY 403 GCTGAATATTGAAGCCGCTATTTCATA 431
Db 301 GAGGAATTGTTAGAACCTATTCTTGCAA 329

RESULT 8

US-10-523-362-1

; Sequence 1, Application US/10523362
; Publication No. US20060064784A1
; GENERAL INFORMATION:
; APPLICANT: Chardonnens, Agnes
; APPLICANT: Puzio, Piotr
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Proteins Associated with Abiotic
; TITLE OF INVENTION: Stress Response
; FILE REFERENCE: 536222010300
; CURRENT APPLICATION NUMBER: US/10/523,362
; CURRENT FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(330)
; OTHER INFORMATION: GRX1
US-10-523-362-1

Query Match 33.2%; Score 143.4; DB 12; Length 333;
Best Local Similarity 64.7%; Pred. No. 6.3e-30;
Matches 213; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 103 ATGGTATCCCAGGAACAGTTGCTCAGTTAAAGGATCTGATTGGCCAAAGGAAGTGT 162
Db 1 ATGGTATCTCAAGAACTATCAAGCAGTCAAGGACCTTATTGCGAAGAACGAGATCTTC 60
QY 163 GTTGCAGCAAGACATACTGCCCTTACTGTAAAGCTACTTTGTCTACCCCTTTTCCAAGAA 222
Db 61 GTCGCATCCAAACGCTACTGTCATCTGCGATGCGCCCTAAACACGCTTTTGAAGAA 120
QY 223 TTGAAGCTTCCCAATCCAAAGCCCTGTGTTGGAATTAGATGAATGACATGCGCTCA 282
Db 121 TTAAGGTTCCCAAGTCCAAAGTCTGTTTTCGAATTGAATGACATGAAGGAAGCGCA 180
QY 283 GAGATTCAAGACGCTTTAGAAGAAATCTCGGGCCAAACAACTGTACTAACGTATACATC 342
Db 181 GACATTCAGGCTGGTTTATATGAGATTAAATGGCCAAAGAACCGTGCACAAACATCTATAT 240
QY 343 AATGGCAAGCACATTTGGTGGTAAACAGCGATTGGAACCTTTGAAGAAAAATGCGCAAGTTA 402
Db 241 AATGGTAAACATATTGAGGCAACGACGACTTTCGAGGAATTGAGGAGACTGCGGAATTG 300
QY 403 GCTGAATATTGAAGCCGCTATTTCATA 431
Db 301 GAGGAATTGTTAGAACCTATTCTTGCAA 329

RESULT 9

US-10-032-585-6780
; Sequence 6780, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6780
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-6780

Query Match 20.6%; Score 89; DB 7; Length 360;

Best Local Similarity 55.4%; Pred. No. 1.7e-14;
Matches 201; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

QY 67 AGAATTATTCGTAAGAGATTTTATCTACTCCAAAATGGTATCCAGGAAACAGTTGCT 126
Db 10 ACATTATTAAACCAAGAGACTATTTCATATCAATCAACAAATGGTTTCATCTCAAGTTAAGAAC 69
QY 127 CAGTAAAGGATCGATTGGCCCAAAAGGAAGTGTGTTGTCAGCAAGACATATCGCCCT 186
Db 70 AAGTCGAACAATTTGATCAAAACCAACACCAAGTTTCATTGCTCCAAATCCTATTGTCCA 129
QY 187 TACTGTAAGCTACTTTGTCTACCTCTTCCAAGATTGAAGCTTCCCAATCCAAGGCC 246
Db 130 TACTGTAAAGCTACCAAAAGCAC-----AATTGAAGCTATATAAACAAGGATGCT 177
QY 247 CTGTGTGTAATTTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTTAGAAGAA 306
Db 178 TACATTTCTGAATTTAGACGAAGTTGACGCGGTGCTGAAATCCAAAGAGCATTTATTGGAA 237
QY 307 ATCTCGGGCCAAAACCTGTACCTAACGTATACATCAATGGCAAGCACATTTGGTGTAAAC 366
Db 238 ATCACTGGTCAAAAGAACCGTTCCAAATGTCCTTTATTGGTGGTCAACATATTGGTGGCAAT 297
QY 367 AGCATTTGGAACCTTTGGAAGAAAATGCAAGTTAGCTGAAATATTGAAGCCGCTATT 426
Db 298 TCCGATGTGCAAGCTTTGAAAGTCTAGTGACAAATTAGATGACAAAATCAAAGCTGCTTTA 357
QY 427 CAA 429
Db 358 TAA 360

RESULT 10
US-10-451-467A-607
; Sequence 607, Application US/10451467A
; Publication No. US20040161840A1
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REEKMAN, RIEKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; TITLE OF INVENTION: YEAST AND FUNGI
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451,467A
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870003.9
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 732
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 607
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-451-467A-607

Query Match 20.6%; Score 89; DB 8; Length 360;
Best Local Similarity 55.4%; Pred. No. 1.7e-14;
Matches 201; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

QY 67 AGAATTATTCGTAAGAGATTTTATCTACTCCAAAATGGTATCCAGGAAACAGTTGCT 126
Db 10 ACATTATTAAACCAAGAGACTATTTCATATCAATCAACAAATGGTTTCATCTCAAGTTAAGAAC 69
QY 127 CAGTAAAGGATCGATTGGCCCAAAAGGAAGTGTGTTGTCAGCAAGACATATCGCCCT 186
Db 70 AAGTCGAACAATTTGATCAAAACCAACACCAAGTTTCATTGCTCCAAATCCTATTGTCCA 129
QY 187 TACTGTAAGCTACTTTGTCTACCTCTTCCAAGATTGAAGCTTCCCAATCCAAGGCC 246
Db 130 TACTGTAAAGCTACCAAAAGCAC-----AATTGAAGCTATATAAACAAGGATGCT 177
QY 247 CTGTGTGTAATTTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTTAGAAGAA 306
Db 178 TACATTTCTGAATTTAGACGAAGTTGACGCGGTGCTGAAATCCAAAGAGCATTTATTGGAA 237
QY 307 ATCTCGGGCCAAAACCTGTACCTAACGTATACATCAATGGCAAGCACATTTGGTGTAAAC 366
Db 238 ATCACTGGTCAAGAACCGTTCCAAATGTCCTTTATTGGTGGTCAACATATTGGTGGCAAT 297
QY 367 AGCATTTGGAACCTTTGGAAGAAAATGCAAGTTAGCTGAAATATTGAAGCCGCTATT 426
Db 298 TCCGATGTGCAAGCTTTGAAAGTCTAGTGACAAATTAGATGACAAAATCAAAGCTGCTTTA 357
QY 427 CAA 429
Db 358 TAA 360

RESULT 11
US-10-425-115-146552
; Sequence 146552, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 146552
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(609)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_65172C.1
US-10-425-115-146552

Query Match 14.1%; Score 61; DB 9; Length 609;
Best Local Similarity 63.1%; Pred. No. 1.9e-06;
Matches 94; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 239 CCAAGGCCCTTGTGTGGAAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTT 298
Db 312 CAAAGTTCTACGCGATTGTGTTGGACCAAGTTGATGACCGGCTCAGTATCCAGTCTACTC 371
QY 299 TAGAAGAAATCTCGGGCCAAAACCTGTACTAACGTATATACATCAATGCAAGCACATTG 358
Db 372 TCGGCGAAATGACTGGCCAGACACCGTACCCAACTCTTCATCGCTCAGAACACATTG 431
QY 359 GTGGTAACAGCGATTGGAACCTTTTGAAG 387
Db 432 GTGGAAACAGCGATTGTCAGTCCCAAGAG 460

RESULT 12
US-10-425-115-149360
; Sequence 149360, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 149360
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_67741C.1
US-10-425-115-149360

Query Match 13.0%; Score 56; DB 9; Length 377;
Best Local Similarity 53.4%; Pred. No. 3.9e-05;
Matches 147; Conservative 0; Mismatches 115; Indels 12; Gaps 1;

QY 126 TCACGTAAAGGATCTGATTGGCCCAAGGAAGTGTGTTCGACGCAAGACATCTGCC 185
DB 94 TAAGGTTCAGCAACTGATTGATGACAAACGGTGTGCGTCTTCAGCAAGAGCTACTGCC 153
QY 186 TTACTGTAAAGTACTTTGTCTACCTCTTCCAAAGAAATTGAACGTTCCCAAAATCCCAAGGC 245
DB 154 GTACTGCAACAACGACGAGCGGCTCTC-----GACGGCTACGGTCCCAAGTA 201
QY 246 CCTGTGTTGGAATTAGATGAATAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAGA 305
DB 202 TGGCAGGTACGAACTGAACAGGAGAGCGACGCGGACGACCTCCAGCAGCGCTTGCTCAA 261
QY 306 AATCTCGGGCCAAAACACTGTACTACGTATACATCAATGGCAACACATTTGGTGTAA 365
DB 262 GATCAGGGGCGAGCGACCGTCTCCCAACGCTTCATCAACAAGCAGCATATTGGTGGCAA 321
QY 366 CACGCAATTTGAAACTTTGAAGAAAATGGCAAG 399
DB 322 CTGGACTTGTAGCGGCTTATTGAACGCGCAAG 355

RESULT 13
US-11-096-568A-26783
; Sequence 26783, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26783
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(578)
; OTHER INFORMATION: Ceres Seq. ID no. 13600582
US-11-096-568A-26783

Query Match 13.0%; Score 56; DB 16; Length 578;
Best Local Similarity 58.3%; Pred. No. 4.8e-05;
Matches 98; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 254 TCGAATTAGATGAATCAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCG 313
DB 182 TTGAGTTGGACACTGAAGAGGATGAAGTGAATCAGTCCTGTGTAATGAGACTG 241
QY 314 GCCAAAAAAGTACCTTAACGTATACATCAATGGCAAGCACATTTGGTGGTAACAGCGATT 373
DB 242 GGCAGGAGACTGTTCCTCAATGTCTTCATCAATGGAACACATTTGGTGGCTGTGACGATA 301

QY 374 TGGAAACTTTGAAGAAAATGCGCAAGTTAGCTGAAATATTGAAGCCGG 421
DB 302 CTATTGCACTGAACAAGGAGGGAAGCTGTTGCTCTCTGCTGACGGAGG 349

RESULT 14
US-10-437-963-29343
; Sequence 29343, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 29343
; LENGTH: 721
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_33855C.1
US-10-437-963-29343

Query Match 12.9%; Score 55.6; DB 8; Length 721;
Best Local Similarity 60.7%; Pred. No. 6.9e-05;
Matches 91; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 254 TCGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCG 313
DB 271 TTGAGTTGGATGGGAGAGTGATGGATCTGAGCTGCGACTTGTGCTGAATGAGACTG 330
QY 314 GCCAAAAAAGTACCTTAACGTATACATCAATGGCAAGCACATTTGGTGGTAACAGCGATT 373
DB 331 GACAAAGGACTGTTCCAAATGCTTCATCAATGGGAAGCATATTGTTGGCTGTGATGATA 390
QY 374 TGGAACTTTGAAGAAAATGCGCAAGTTAG 403
DB 391 CTTTGGCATTGAACAATGAAGGGAAGCTGG 420

RESULT 15
US-10-523-362-47
; Sequence 47, Application US/10523362
; Publication No. US20060064784A1
; GENERAL INFORMATION:
; APPLICANT: Chardonens, Agnes
; APPLICANT: Puzio, Piotr
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Proteins Associated with Abiotic
; TITLE OF INVENTION: Stress Response
; FILE REFERENCE: 532622010300
; CURRENT APPLICATION NUMBER: US/10/523,362
; CURRENT FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 47
; LENGTH: 733
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)..(466)
; OTHER INFORMATION: OZ1116C2194
US-10-523-362-47

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OM protein - protein search, using sw model

Run on: November 6, 2006, 19:08:05 ; Search time 200 Seconds
(without alignments)

326.910 Million cell updates/sec

Title: US-10-523-362-4

Perfect score: 714

Sequence: 1 METNFSFDSNLIVIIITLF.....DLETLKNGKLBIKPVFQ 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq.8.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	714	100.0	143	5	ABG93088 S. cerevi
2	714	100.0	143	8	Adk90659 Baker's Y
3	714	100.0	143	8	Adt87075 Yeast Str
4	391	54.8	110	5	ABG93054 S. cerevi
5	391	54.8	110	8	Adk90657 Baker's Y
6	300.5	42.1	119	5	ABG93325 C. albica
7	300.5	42.1	119	5	ABP73943 Candida a
8	216	30.3	136	8	Adk90701 Rice oxid
9	215.5	30.2	127	8	Adk90703 Rice oxid
10	215	30.1	133	3	AGI15306 Arabidops
11	215	30.1	135	3	AGI15305 Arabidops
12	215	30.1	135	8	Adk90687 Thale cre
13	215	30.1	147	3	AGI15304 Arabidops
14	214.5	30.0	133	8	Adk90677 Rape oxid
15	212	29.7	102	8	ADR86373 Aspergill
16	210	29.4	133	3	AGI11727 Arabidops
17	210	29.4	135	3	AGI11726 Arabidops
18	210	29.4	152	3	AGI11725 Arabidops
19	209	29.3	119	5	ABG60108 Human DIT
20	207.5	29.1	173	8	Adk90675 Rape oxid
21	206	28.9	109	3	AGI45926 Arabidops
22	206	28.9	109	3	AGI09195 Arabidops
23	206	28.9	109	3	AGI06665 Arabidops

24	206	28.9	111	3	AGI09194 Arabidops
25	206	28.9	111	3	AGI45925 Arabidops
26	206	28.9	111	3	AGI06664 Arabidops
27	206	28.9	111	8	Adk90683 Thale cre
28	204	28.6	120	8	Adk90671 Rape oxid
29	203.5	28.5	122	3	AGI4252 Arabidops
30	203.5	28.5	125	3	AGI4251 Arabidops
31	203.5	28.5	126	3	AGI33583 Arabidops
32	203.5	28.5	129	3	AGI33582 Arabidops
33	203	28.4	116	3	AGI04253 Arabidops
34	203	28.4	120	3	AGI33584 Arabidops
35	199	27.9	109	3	AGI35055 Arabidops
36	199	27.9	111	3	AGI35054 Arabidops
37	199	27.9	154	3	AGI43269 Arabidops
38	199	27.9	169	3	AGI43268 Arabidops
39	199	27.9	179	3	AGI43267 Arabidops
40	199	27.9	179	8	Adk90689 Thale cre
41	198.5	27.8	122	3	AGI46499 Arabidops
42	198.5	27.8	122	3	AGI46496 Arabidops
43	198.5	27.8	125	3	AGI46498 Arabidops
44	198.5	27.8	125	3	AGI46495 Arabidops
45	198	27.7	111	8	Adk90681 Thale cre

ALIGNMENTS

RESULT 1

ABG93088
ID ABG93088 standard; protein; 143 AA.

XX AC ABG93088;

XX DT 21-NOV-2002 (first entry)

XX DE S. cerevisiae BAX-associated protein fragment SEQ ID 134.

XX KW Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
XX KW vasotrophic; vaccine; gene therapy; proliferative disorder; cancer;
XX KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
XX KW neurodegeneration; cell death.

XX OS Saccharomyces cerevisiae.

XX PN WO200264766-A2.

XX PD 22-AUG-2002.

XX PF 21-DEC-2001; 2001WO-BP015398.

XX PR 22-DEC-2000; 2000EP-00870318.

XX PR 04-JAN-2001; 2001EP-00870002.

XX PR 09-JAN-2001; 2001EP-00870003.

XX PA (JANC) JANSSEN PHARM NV.

XX PI Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;

XX DR WPI; 2002-667002/71.

XX DR N-PSDB; ABQ76354.

XX XX New isolated nucleic acid representing a synthetic BAX-gene, useful as
XX XX medicament for treating, preventing and/or alleviating yeast or fungal
XX XX infections or proliferative disorders, or for preventing apoptosis in
XX XX certain diseases.

XX XX Claim 36; Fig 1; 344pp; English.

XX CC This invention describes a novel nucleic acid representing a synthetic
XX CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
XX CC resistant yeast or fungi, identifying, or obtaining and identifying
XX CC Candida spp. sequences that are differentially expressed in a pathway
XX CC eventually leading to programmed cell death or identifying inhibitors or

CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide, immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenic flora of humans and
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polypeptide associated with the Bax gene
CC described in the disclosure of the invention
XX
SQ Sequence 143 AA;

Query Match 100.0%; Score 714; DB 5; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.1e-71;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFSFDSNLIVIIITLFAIRIIAKRFLSTPKMVSQETVAHVKDILGOKEVFVAAKTY 60
DB 1 METNFSFDSNLIVIIITLFAIRIIAKRFLSTPKMVSQETVAHVKDILGOKEVFVAAKTY 60

QY 61 CPYCKATLSTLFOELNVPKSKALVLEDEMSNGSEIQDALEESGQKTPNVYINGKHI 120
DB 61 CPYCKATLSTLFOELNVPKSKALVLEDEMSNGSEIQDALEESGQKTPNVYINGKHI 120

QY 121 GNSDLETLKNGKLAELIKPVFQ 143
DB 121 GNSDLETLKNGKLAELIKPVFQ 143

RESULT 2
ADK90659
ID ADK90659 standard; protein; 143 AA.
XX
AC ADK90659;
XX
DT 20-MAY-2004 (first entry)
XX
DE Baker's yeast glutaredoxin 2 (GRX2) protein SeqID 4.
XX
KW baker's yeast; GRX2; transgenic; abiotic stress response; crop plant;
KW oxidoreductase stress-related protein; ORSRP; environmental stress;
KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
KW thiodoxin; THX; Quantitative trait locus; QTL.
XX
OS Saccharomyces cerevisiae.
XX
PN WO2004018687-A2.
XX
PD 04-MAR-2004.
XX
PF 01-JUL-2003; 2003WO-EP006994.
XX
PR 07-AUG-2002; 2002EP-00017671.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
XX Chardonnens A, Puzio P;
PI Mckersie B, Chen R;
DR WPI; 2004-226856/21.
DR N-PSDB; ADK90659.
XX
XX New transgenic plant cell transformed by oxidoreductase stress-related
PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
PT plant with increased environmental stress tolerance.
XX
PS Example 2; SEQ ID NO 4; 140pp; English.
XX

CC This invention relates to novel transgenic plant cells transformed by
CC genes encoding proteins associated with the abiotic stress response.
CC Specifically, it refers to transgenic crop plants expressing the
CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
CC increased tolerance and/or resistance to environmental stresses such as
CC salinity, drought, temperature, chemicals or pathogens. The present
CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/or
CC thiodoxin (THX) proteins, where expression is under the control of an
CC inducible tissue-specific or developmentally-specific promoter and
CC furthermore it provides antisense oligos and RNA interference molecules
CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
CC associated with environmental stress tolerance. This polypeptide sequence
CC is a baker's yeast GRX protein of the invention.
XX
SQ Sequence 143 AA;

Query Match 100.0%; Score 714; DB 8; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.1e-71;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFSFDSNLIVIIITLFAIRIIAKRFLSTPKMVSQETVAHVKDILGOKEVFVAAKTY 60
DB 1 METNFSFDSNLIVIIITLFAIRIIAKRFLSTPKMVSQETVAHVKDILGOKEVFVAAKTY 60

QY 61 CPYCKATLSTLFOELNVPKSKALVLEDEMSNGSEIQDALEESGQKTPNVYINGKHI 120
DB 61 CPYCKATLSTLFOELNVPKSKALVLEDEMSNGSEIQDALEESGQKTPNVYINGKHI 120

QY 121 GNSDLETLKNGKLAELIKPVFQ 143
DB 121 GNSDLETLKNGKLAELIKPVFQ 143

RESULT 3
ADT87075
ID ADT87075 standard; protein; 143 AA.
XX
AC ADT87075;
XX
DT 13-JAN-2005 (first entry)
XX
DE Yeast Stress-related protein from gene YEL045C.
XX
KW Yeast; Stress-related protein; SRP; environmental stress; abiotic stress;
KW drought; heat; cold; salt.
XX
OS Saccharomyces cerevisiae.
XX
PN WO2004092398-A2.
XX
PD 28-OCT-2004.
XX
PF 15-APR-2004; 2004WO-US011888.
XX
PR 15-APR-2003; 2003EP-00080800.
PR 02-MAY-2003; 2003EP-00039728.
PR 01-AUG-2003; 2003EP-00016672.
PR 30-SEP-2003; 2003EP-00022225.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
XX Puzio P, Chardonnens A, Shirley A, Wang X, Sarria-Millan R;
PI Mckersie B, Chen R;
DR WPI; 2004-766883/75.
DR N-PSDB; ADT87074.
XX
XX New isolated nucleic acid molecule comprises a sequence encoding Stress-
PT Related Protein (SRP), useful for producing transformed plants with
PT altered metabolic activity resulting in increased tolerance or resistance
PT to environmental stress.
PT

Claim 15; SEQ ID NO 53; 911bp; English.

The invention relates an isolated nucleic acid molecule comprises a nucleic acid molecule encoding a Stress-Related Protein (SRP) from Yeast or E. coli and their homologues from Rice, Soybean and Rape. Also included are a transformed plant cell with altered metabolic activity compared to a corresponding non-transformed wild type plant cell (where the metabolic activity is altered by transformation with a SRP coding nucleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell), a transgenic plant generated from the plant cell above (and which is a monocot or dicot plant, or a gymnosperm plant), a seed produced by a transgenic plant above (where the seed is genetically homozygous for a transgene conferring altered metabolic activity resulting in an increased tolerance to environmental stress as compared to a corresponding non-transformed wild type plant), a nucleic acid construct which confers the expression of the nucleic acid molecule above (comprising one or more regulatory elements, where expression of the SRP coding nucleic acid in a host cell results in altered metabolic activity resulting in increased tolerance to environmental stress as compared to a corresponding non-transformed wild type host cell), a vector comprising the nucleic acid molecule above or the nucleic acid construct, a host cell which has been transformed stably or transiently with the vector (or the nucleic acid molecules above, or the nucleic acid construct), an isolated Stress Related Protein (SRP) selected from the amino acid sequences fully given in the specification and/or its homologues, a method of producing a transgenic plant with altered metabolic activity compared to a corresponding non-transformed wild type plant cell, modifying stress tolerance of a plant, detecting environmental stress in plant cells or plants, screening plant cells or plants for increased tolerance and/or resistance to environmental stress, breeding plant cells or plants towards increased tolerance and/or resistance to environmental stress, increasing tolerance of a plant to at least one abiotic stress, a plant transformed with the nucleic acids above and a seed of the plant. The altered metabolic activity and/or a SRP encoding nucleic acids or its homologues are useful as markers for selection of plants or plant cells with increased tolerance to environmental stress, or for detection of stress in plants or plant cells. The nucleic acids are useful for producing transformed plants with altered metabolic activity resulting in increased tolerance and/or resistance to an environmental stress (drought, heat, cold and salt) as compared to a corresponding non-transformed wild-type plant cell. The present sequence is a yeast SRP of the invention.

Sequence 143 AA;

Query Match 100.0%; Score 714; DB 8; Length 143;

Best Local Similarity 100.0%; Pred. No. 1.1e-71;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METNFSNLSNLIIVIIITLPTRIIAKRLSTPKMVSQETVAHVKDLIGQKEVFVAQTY 60

Db 1 METNFSNLSNLIIVIIITLPTRIIAKRLSTPKMVSQETVAHVKDLIGQKEVFVAQTY 60

Qy 61 CPYCKATLTLFQELNVPKSKALVLEIDENSGSEIQDALEEISGQKTPNVYINGKHIG 120

Db 61 CPYCKATLTLFQELNVPKSKALVLEIDENSGSEIQDALEEISGQKTPNVYINGKHIG 120

Qy 121 GNSDLETLKNGKLAELKPVFQ 143

Db 121 GNSDLETLKNGKLAELKPVFQ 143

RESULT 4

ABG93054

ID ABG93054 standard; protein; 110 AA.

XX AC ABG93054;

XX DT 21-NOV-2002 (first entry)

XX DE S. cerevisiae BAX-associated protein fragment SEQ ID 66.

XX

KW Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KW neurodegeneration; cell death.

XX Saccharomyces cerevisiae.

XX WO200264766-A2.

XX 22-AUG-2002.

XX 21-DEC-2001; 2001WO-EP015398.

XX 22-DEC-2000; 2000EP-00870318.

PR 04-JAN-2001; 2001EP-00870002.

PR 09-JAN-2001; 2001EP-00870003.

XX (JANC) JANSSEN PHARM NV.

PA Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;

PI WPI: 2002-667002/71.

DR N-PSDB; ABQ76320.

XX New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medicament for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.

XX Claim 36; Fig 1, 344pp; English.

XX This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide; immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenic flora of humans and
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polypeptide associated with the Bax gene
CC described in the disclosure of the invention

XX Sequence 110 AA;

Query Match 54.8%; Score 391; DB 5; Length 110;

Best Local Similarity 64.5%; Pred. No. 1.5e-35;

Matches 69; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

Qy 35 MVSQETVAHVKDLIGQKEVFVAQTYCPYCKATLTLFQELNVPKSKALVLEIDENSGS 94

Db 1 MVSQETIKHVKDLIAENEIFVASKTYCPYCHAAINTLFEKLVPRSKVLQLNDMKEGA 60

Qy 95 EIODALEEISGQKTPNVYINGKHIGNSDLETLKNGKLAELKPV 141

Db 61 DIOALYEINGQKTPNVYINGKHIGNSDLETLKNGKLAELKPV 107

RESULT 5

ADK90657

ID ADK90657 standard; protein; 110 AA.

XX AC ADK90657;

XX

DT 20-MAY-2004 (first entry)
 XX Baker's yeast glutaredoxin 1 (GRX1) protein SeqID 2.
 DE
 XX baker's yeast; GRX1; transgenic; abiotic stress response; crop plant;
 KW oxidoreductase stress-related protein; ORSRP; environmental stress;
 KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
 KW thiorodoxin; THX; Quantitative Trait Locus; QTL.
 XX
 OS Saccharomyces cerevisiae.
 XX
 XX WO2004018687-A2.
 PN
 XX 04-MAR-2004.
 PD
 XX
 PF 01-JUL-2003; 2003WO-EP006994.
 XX
 XX 07-AUG-2002; 2002EP-00017671.
 PR
 XX (BADI) BASF PLANT SCI GMBH.
 PA
 XX Chardonnais A, Puzio P;
 PI
 XX WPI; 2004-226856/21.
 DR N-PSDB; ADK90656.
 DR
 XX New transgenic plant cell transformed by oxidoreductase stress-related
 PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
 PT plant with increased environmental stress tolerance.
 PT
 XX
 XX Example 2; SEQ ID NO 2; 140pp; English.
 PS
 XX This invention relates to novel transgenic plant cells transformed by
 CC genes encoding proteins associated with the abiotic stress response.
 CC Specifically, it refers to transgenic crop plants expressing the
 CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
 CC increased tolerance and/ or resistance to environmental stresses such as
 CC salinity, drought, temperature, chemicals or pathogens. The present
 CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/ or
 CC thiorodoxin (THX) proteins, where expression is under the control of an
 CC inducible tissue-specific or developmentally-specific promoter and
 CC furthermore it provides antisense oligos and RNA interference molecules
 CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
 CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
 CC associated with environmental stress tolerance. This polypeptide sequence
 CC is a baker's yeast GRX protein of the invention.
 XX
 SQ Sequence 110 AA;
 Query Match 54.8%; Score 391; DB 8; Length 110;
 Best Local Similarity 64.5%; Pred. No. 1.5e-35;
 Matches 69; Conservative 23; Mismatches 15; Indels 0; Gaps 0;
 QY 35 MVSQETVAHVVDLIGQKEVFAAKTCPCYKATLSTLFOELNVPKSKALVLELDENSGS 94
 DB 1 MVSQETIKHKVDLTAENEIVASKTCPCYCHALNTLFKELKVPKSKVLQLNDMKEGA 60
 QY 95 EIQDALIEISGQKTPNVNYNGHIGNSDLETKKNGKLAELIKPV 141
 DB 61 DIQAALYEINGQRTVPVNYINGKHIGGNDLQELRENGELELELPI 107
 RESULT 6
 ABG93325
 ID ABG93325 standard; protein; 119 AA.
 XX
 AC ABG93325;
 XX
 DT 21-NOV-2002 (first entry)
 XX
 XX C. albicans BAX-associated protein fragment SEQ ID 608.
 DE
 XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
 • KW

KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
 KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
 KW neurodegeneration; cell death.
 XX
 OS Candida albicans.
 XX
 XX WO200264766-A2.
 PN
 XX 22-AUG-2002.
 PD
 XX
 XX 21-DEC-2001; 2001WO-EP015398.
 PF
 XX 22-DEC-2000; 2000EP-00870318.
 PR 04-JAN-2001; 2001EP-00870002.
 PR 09-JAN-2001; 2001EP-00870003.
 XX
 PA (JANC) JANSSEN PHARM NV.
 XX
 XX Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;
 PI
 XX WPI; 2002-667002/71.
 DR N-PSDB; ABQ76591.
 DR
 XX New isolated nucleic acid representing a synthetic BAX-gene, useful as
 PT medicament for treating, preventing and/or alleviating yeast or fungal
 PT infections or proliferative disorders, or for preventing apoptosis in
 PT certain diseases.
 PT
 XX Claim 36; Fig 2; 344pp; English.
 PS
 XX This invention describes a novel nucleic acid representing a synthetic
 CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
 CC resistant yeast or fungi, identifying, or obtaining and identifying
 CC Candida spp. sequences that are differentially expressed in a pathway
 CC eventually leading to programmed cell death or identifying inhibitors or
 CC inhibitor sequences of Bax-induced cell death. The products of the
 CC invention have cytostatic, fungicide, immunosuppressive, virucide and
 CC vasotropic activity and can be used in vaccines or for gene therapy. The
 CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
 CC antisense molecules and antibodies are useful as medicaments or in
 CC preparing a medicament for treating, preventing and/or alleviating
 CC diseases associated with yeast or fungi or proliferative disorders, such
 CC as cancer, or for preventing apoptosis in certain diseases. The compounds
 CC or polypeptides, or the genetically modified organism are useful for
 CC preparing a medicament for modifying the endogenous flora of humans and
 CC other mammals. The vaccine is useful for immunising against yeast or
 CC fungal infections. Apoptosis-related diseases include autoimmune disease,
 CC ischaemia, diseases related with viral infections or neurodegenerations.
 CC This sequence represents a polypeptide associated with the Bax gene
 CC described in the disclosure of the invention
 XX
 SQ Sequence 119 AA;
 Query Match 42.1%; Score 300.5; DB 5; Length 119;
 Best Local Similarity 50.4%; Pred. No. 2.5e-25;
 Matches 61; Conservative 24; Mismatches 31; Indels 5; Gaps 2;
 QY 19 LFATRIIAKRFSLTPKMSQETVAHVVDLIGQKEVFAAKTCPCYKATLSTLFOELNVP 78
 DB 1 MFRT-LLTKRLFTSTWSSQVKNKVEQLIKTPFIASKSYCPYCKATKST----IEAI 55
 QY 79 KSKALVLELDENSGSEIQDALIEISGQKTPNVNYNGHIGNSDLETKKNGKLAEL 138
 DB 56 TKDAVILELDEVDGAIEQALLETITGQRTVPVNYFGGQHQHIGNSDVQALKSKDLDDKI 115
 QY 139 K 139
 DB 116 K 116
 RESULT 7
 ABP73943
 ID ABP73943 standard; protein; 119 AA.

XX ABP73943;
XX 30-JAN-2003 (first entry)
XX Candida albicans essential protein SEQ ID NO 7780.
XX Fungus; Yeast; tetracycline; promoter; GRACE strain; biosynthesis;
XX signal transduction; DNA replication; cell division; growth;
XX proliferation; Candida albicans; fungicide; antifungal.
XX Candida albicans.
XX WO200253728-A2.
XX 11-JUL-2002.
XX 26-DEC-2001; 2001WO-US049486.
XX 29-DEC-2000; 2000US-0259128P.
XX 20-FEB-2001; 2001US-00792024.
XX 22-AUG-2001; 2001US-0314050P.
XX (ELIT-) ELITRA PHARM INC.
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX WPI; 2002-566694/60.
XX N-PSDB; AB232493.
XX Constructing strains for identifying gene products as effective targets
XX for therapeutic intervention, by inactivating in the strain one allele of
XX a gene and placing other allele of the gene under conditional expression.
XX Claim 44; SEQ ID NO 7780; 167pp + Sequence Listing; English.
XX The invention relates to constructing (M1) a strain of diploid fungal
XX cells in which both alleles of a gene are modified, comprising modifying
XX one allele by insertion or replacement by a cassette having an
XX expressible selectable marker and modifying other allele by
XX recombination, of a promoter replacement fragment with a heterologous
XX promoter, so that expression of the second allele is regulated by the
XX promoter. (M1) is useful for constructing a strain of diploid fungal
XX cells in which both alleles of a gene are modified. The diploid fungal
XX cells having both alleles modified are useful for identifying a gene that
XX is essential to the survival or growth of a fungus, a gene that
XX contributes to the virulence and/or pathogenicity of a fungus, a gene
XX that contributes to the resistance of a diploid fungus to an antifungal
XX agent, an antifungal agent that inhibits the growth of a diploid fungus
XX and for identifying a therapeutic agent for treatment of a mammalian
XX disease. (M1) is useful for identifying a compound which modulates the
XX activity of a gene product, preferably enzymatic activity, carbon
XX compound catabolism, biosynthetic, transporter, transcriptional,
XX translational, signal transduction, DNA replication and cell division
XX activity. The method is useful for identifying a compound having the
XX ability to inhibit growth or proliferation of C. albicans cells and for
XX treating infection by C. albicans. The present sequence is that of an
XX essential Candida albicans protein used in the method of the invention.
XX Note: The sequence data for this patent is not represented in the printed
XX specification but is based on sequence information supplied to Derwent by
XX the European Patent Office
XX
XX Sequence 119 AA;
Query Match 42.1%; Score 300.5; DB 5; Length 119;
Best Local Similarity 50.4%; Pred. No. 2.5e-25;
Matches 61; Conservative 24; Mismatches 31; Indels 5; Gaps 2;
QY 19 LPATRIAKRFLSTPKNVQSVETVAHVVDLIGQKEVFAAKTCYPCYKATLSTLFOELNVP 78
DB 1 MFRT-LITKRLFTNTMWSQVKNVQLEIKTRPVFIASKSCYPCYKATSKT-----IEAI 55
QY 79 KSAVLVLEDEMSGSEIQDALEBISGQKTPVNPVYINGKHIGGNSDLETCLKNGKLAEL 138

DB 56 TKDAVILELDEVDGAEIQEALLETGQRTVNFVIGGQHGHSVDQALKSDKDDKI 115
QY 139 K 139
DB 116 K 116
RESULT 8
ADK90701
ID ADK90701 standard; protein; 136 AA.
XX AC ADK90701;
XX 20-MAY-2004 (first entry)
XX DE Rice oxidoreductase stress-related protein OZ1116C12744 SeqID 46.
XX rice; transgenic; abiotic stress response; crop plant;
XX oxidoreductase stress-related protein; ORSRP; environmental stress;
XX salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
XX thioredoxin; THX; Quantitative Trait Locus; QTL.
XX Oryza sativa.
XX WO2004018687-A2.
XX 04-MAR-2004.
XX 01-JUL-2003; 2003WO-BF006994.
XX 07-AUG-2002; 2002EP-00017671.
XX (BADI) BASF PLANT SCI GMBH.
XX Chardonnais A, Puzio P;
XX WPI; 2004-226856/21.
XX N-PSDB; ADK90700.
XX New transgenic plant cell transformed by oxidoreductase stress-related
XX protein (ORSRP) coding nucleic acid, useful for producing a transgenic
XX plant with increased environmental stress tolerance.
XX Example 2; SEQ ID NO 46; 140pp; English.
XX This invention relates to novel transgenic plant cells transformed by
XX genes encoding proteins associated with the abiotic stress response.
XX Specifically, it refers to transgenic crop plants expressing the
XX heterologous oxidoreductase stress-related protein (ORSRP) that confers
XX increased tolerance and/or resistance to environmental stresses such as
XX salinity, drought, temperature, chemicals or pathogens. The present
XX invention describes the ORSRPs as heat-scable glutaredoxin (GRX) and/or
XX thioredoxin (THX) proteins, where expression is under the control of an
XX inducible tissue-specific or developmentally-specific promoter and
XX furthermore it provides antisense oligos and RNA interference molecules
XX to inhibit ORSRP expression. In addition, these nucleic acids are useful
XX as Quantitative Trait Locus (QTL) markers that can map genetic loci
XX associated with environmental stress tolerance. This polypeptide sequence
XX is a rice ORSRP protein of the invention.
XX
XX Sequence 136 AA;
Query Match 30.3%; Score 216; DB 8; Length 136;
Best Local Similarity 37.3%; Pred. No. 9.4e-16;
Matches 44; Conservative 30; Mismatches 42; Indels 2; Gaps 2;
QY 21 ATRIATKRLSTPKNVQSVETVAHVVDLIGQKEVFAAKTCYPCYKATLSTLFOELNVPKS 80
DB 13 AALIALAALGAASGATSKSFVSTVKAHDVIFSKSCYPCYCRRA-KAVFKELEL-KK 70
QY 81 KALVLVLEDEMSGSEIQDALEBISGQKTPVNPVYINGKHIGGNSDLETCLKNGKLAEL 138


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PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140335P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140981P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142300P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
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PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147193P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
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PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.

PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 28-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
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PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 14-OCT-1999; 99US-0159329P.
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PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
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PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 30.1%; Score 215; DB 3; Length 133;
Best Local Similarity 38.3%; Pred. No. 1.2e-15;
Matches 51; Conservative 28; Mismatches 42; Indels 12; Gaps 4;
QY 7 FDSNLVITLITLIPATRIIAKRFSLTPKMWVSOETVAHVXDLICQKEVFAAKTYCPYCKA 66
Db 2 FRISIMVLLVALVTFTISMVSSAASPE-----ADFKVKTITSHKIVIPSKSYCPYCKK 55
QY 67 TLSTLFOELN-VPKSKALVLELDEMNGSEIQDALEISQKTPVNVYINGKHIGNSDL 125
Db 56 AKS-VFRELDQVB-----YVVELDEREDGWSIQTALGEIVGRRTVPQVFINGRHLGSSDDT 110
QY 126 ETLKXNGKLAAIL 138
Db 111 VDAYSGLAKL 123

RESULT 11
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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151085P.
PR 27-AUG-1999; 99US-0151086P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

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Query Match 30.1%; Score 215; DB 3; Length 135;
Best Local Similarity 38.3%; Pred. No. 1.2e-15;
Matches 51; Conservative 28; Mismatches 42; Indels 12; Gaps 4;

Qy 7 FDSNLVILIIITLPATRIIAKRLSTPKMWSQETVAHVKDILIGQKEVFAAKTCYCYCKA 66
Db 4 FRISWMVLLVALVTFISMVSSAASPE-----ADPVKKTISHKIVIFSKSYCYCKK 57

Qy 67 TLSTLFOELN-VPKSKALVLEDEMNGSEIQDALEISQKTVPNVYINGKHIGGNSDL 125
Db 58 AKS-VFRELQV-----YVVELDEREDGWSIQTALGEIVGRRTVPQVFINGKHLGGSDDT 112

Qy 126 ETLKNGKLAEL 138
Db 113 VDYESGELAKLL 125

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```

RESULT 12
ADK90687
ID ADK90687 standard; protein; 135 AA.
XX
AC ADK90687;
XX
DT 20-MAY-2004 (first entry)
XX
DE Thale cress oxidoreductase stress-related protein AtQ9M457 SeqID 32.
XX
KW thale cress; transgenic; abiotic stress response; crop plant;
KW oxidoreductase stress-related protein; ORSRP; environmental stress;
KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
KW thioredoxin; THX; Quantitative Trait Locus; QTL.
XX
OS Arabidopsis thaliana.
XX
PN W02004018687-A2.
XX
PD 04-MAR-2004.
XX
PF 01-JUL-2003; 2003WO-EP006994.
XX
PR 07-AUG-2002; 2002EP-00017671.
XX
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Chardonnais A, Puzio P;
XX
WP1; 2004-226856/21.
DR N-PSDB; ADK90686.
XX
XX New transgenic plant cell transformed by oxidoreductase stress-related
PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
PT plant with increased environmental stress tolerance.
XX
PS Example 2; SEQ ID NO 32; 140pp; English.
XX
XX This invention relates to novel transgenic plant cells transformed by
CC genes encoding proteins associated with the abiotic stress response.
CC Specifically, it refers to transgenic crop plants expressing the
CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
CC increased tolerance and/or resistance to environmental stresses such as
CC salinity, drought, temperature, chemicals or pathogens. The present
CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/or
CC thioredoxin (THX) proteins, where expression is under the control of an
CC inducible tissue-specific or developmentally-specific promoter and
CC furthermore it provides antisense oligos and RNA interference molecules
CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
CC associated with environmental stress tolerance. This polypeptide sequence
CC is a thale cress ORSRP protein of the invention.
XX
SQ Sequence 135 AA;

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Query Match 30.1%; Score 215; DB 8; Length 135;
Best Local Similarity 38.3%; Pred. No. 1.2e-15;
Matches 51; Conservative 28; Mismatches 42; Indels 12; Gaps 4;

Qy 7 FDSNLVILIIITLPATRIIAKRLSTPKMWSQETVAHVKDILIGQKEVFAAKTCYCYCKA 66
Db 4 FRISWMVLLVALVTFISMVSSAASPE-----ADPVKKTISHKIVIFSKSYCYCKK 57

Qy 67 TLSTLFOELN-VPKSKALVLEDEMNGSEIQDALEISQKTVPNVYINGKHIGGNSDL 125
Db 58 AKS-VFRELQV-----YVVELDEREDGWSIQTALGEIVGRRTVPQVFINGKHLGGSDDT 112

Qy 126 ETLKNGKLAEL 138
Db 113 VDYESGELAKLL 125

RESULT 13

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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151085P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
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PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 22-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 30.18; Score 215; DB 3; Length 147;
Best Local Similarity 38.3%; Pred. No. 1.4e-15;
Matches 51; Conservative 28; Mismatches 42; Indels 12; Gaps 4;

QY 7 FDSNLIVIIITLIPATRIIAKRLFLSTPKMVSQETVAHVKDLIGQKEVFVAAKTVCYCKA 66
DB 16 FRISWMLLVALVTFISMVSSRAASPE-----ADPVKTTISHKIVIFSCKYCPYCKK 69
QY 67 TLSTLFOELN-VPKSKALVLELDEMNSGSIQDALEISGQKTPVNVYINGKHIGNSDL 125
DB 70 AKS-VFRELQVPH---YVVELDEREDGWSIQTALGSEIVGRRTVPQVFINGKILGSDDT 124
QY 126 ETLKNGKLAAIL 138
DB 125 VDYESGELAKLL 137

RESULT 15
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RESULT 14
ADK90677
ID ADK90677 standard; protein; 133 AA.
XX
AC ADK90677;
XX
DT 20-MAY-2004 (first entry)
XX
DE Rape oxidoreductase stress-related protein BN1106C2582 SeqID 22.
XX
KW rape; transgenic; abiotic stress response; crop plant;
KW oxidoreductase stress-related protein; ORSRP; environmental stress;
KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
KW thioredoxin; THX; Quantitative Trait Locus; QTL.
XX
OS Brassica napus.
XX
PN WO2004018687-A2.
XX
PD 04-MAR-2004.
XX
PF 01-JUL-2003; 2003WO-EP006994.
XX
PR 07-AUG-2002; 2002EP-00017671.
XX
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Chardonnais A, Puzio P;
XX
WP1; 2004-226856/21.
DR N-PSDB; ADK90676.
XX
XX New transgenic plant cell transformed by oxidoreductase stress-related
PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
PT plant with increased environmental stress tolerance.
XX
PS Example 2; SEQ ID NO 22; 140pp; English.
XX
XX This invention relates to novel transgenic plant cells transformed by
CC genes encoding proteins associated with the abiotic stress response.
CC Specifically, it refers to transgenic crop plants expressing the
CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
CC increased tolerance and/ or resistance to environmental stresses such as
CC salinity, drought, temperature, chemicals or pathogens. The present
CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/ or
CC thioredoxin (THX) proteins, where expression is under the control of an
CC inducible tissue-specific or developmentally-specific promoter and
CC furthermore it provides antisense oligos and RNA interference molecules
CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
CC associated with environmental stress tolerance. This polypeptide sequence
CC is a rape ORSRP protein of the invention.
XX
SQ Sequence 133 AA;

Query Match 30.0%; Score 214.5; DB 8; Length 133;
Best Local Similarity 36.7%; Pred. No. 1.3e-15;
Matches 51; Conservative 30; Mismatches 41; Indels 17; Gaps 5;

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DB 3 MMSFSS-----MAMLLVALVSSISIVSSASSPE-----AEFVKTTISHKIVIFSCKY 51
QY 61 CPYCKATLSTLFOELN-VPKSKALVLELDEMNSGSIQDALEISGQKTPVNVYINGKHI 119
DB 52 CPTCREAKS-VFSELQVPH---YVVELDEREDGWNVSALGSEIVGRRTVPQVFINGKHI 106
QY 120 GNSDLETLKNGKLAAIL 138
DB 107 GGSDDTVFAHESGELAKLL 125

RESULT 15
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2006, 03:36:27 ; Search time 182 Seconds
(without alignments)
4605.624 Million cell updates/sec

Title: US-10-523-362-3
Perfect score: 432
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Gapop 10.0 , Gapext 1.0

Searched: 2461376 seqs, 970166171 residues

Total number of hits satisfying chosen parameters: 4922752

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	432	100.0	432	8	US-11-217-529-76174
2	432	100.0	432	8	US-11-251-208-52
3	336.6	77.9	570	8	US-11-217-529-3898
4	153.8	35.6	345	8	US-11-217-529-3588
5	146.6	33.9	333	8	US-11-217-529-75707
6	56	13.0	378	6	US-10-953-349-37584
7	55.6	12.9	575	6	US-10-449-902-15440
8	55.6	12.9	729	6	US-10-449-902-4892
9	55	12.7	392	6	US-10-449-902-279
10	55	12.7	885	9	US-11-218-305-2985
11	53.2	12.3	597	8	US-11-216-545-6672
12	49.4	11.4	568	6	US-10-953-349-14823
13	49.2	11.4	695	6	US-10-953-349-20411
14	49.2	11.4	894	9	US-11-218-305-4450
15	47.2	10.9	790	6	US-10-449-902-17381
16	47	10.9	282	8	US-11-217-529-79774
17	46.8	10.8	385	7	US-11-314-834-1485
18	46.8	10.8	590	7	US-11-292-078-8409
19	46.4	10.7	529	7	US-11-314-834-628
20	45.6	10.6	844	9	US-11-218-305-2209
21	45	10.4	550	7	US-11-292-078-16761
22	44.8	10.4	693	6	US-10-953-349-28950
23	43.8	10.1	343	7	US-11-292-078-4027

ALIGNMENTS

RESULT 1
US-11-217-529-76174
; Sequence 76174, Application US/11217529
; Publication No. US2006099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIOHRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76174
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76174
Query Match 100.0%; Score 432; DB 8; Length 432;
Best Local Similarity 100.0%; Pred. No. 2.6e-120;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGACCAATTTTTCCTTCGACTCGAATTTTAAATTTGTTTATTTATCATTTACGCTGTTT 60
DB 1 ATGAGACCAATTTTTCCTTCGACTCGAATTTTAAATTTGTTTATTTATCATTTACGCTGTTT 60
QY 61 GCCACAAGAAATTTGCTAAAAGATTTTATCTACTCCAAAATTTGTTATCCAGGAACA 120
DB 61 GCCACAAGAAATTTGCTAAAAGATTTTATCTACTCCAAAATTTGTTATCCAGGAACA 120
QY 121 GTTGCTCAGTAAGATCTGATGCGCAAGAGATGTTGTTGTCAGCAAGACATAC 180
DB 121 GTTGCTCAGTAAGATCTGATGCGCAAGAGATGTTGTTGTCAGCAAGACATAC 180
QY 181 TGGCCTTACTGTAAGACTTTGTTCTACCTCTTCCAGAAATTTGACGTTCCCAATCC 240
DB 181 TGGCCTTACTGTAAGACTTTGTTCTACCTCTTCCAGAAATTTGACGTTCCCAATCC 240
QY 241 AAGGCCCTTGTGTTGGAATTAGATGAAATGAGCAATGGCTCAGAGATTCAAGCGCTTTA 300

Db	241	AAGGCCCTTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA	300
Qy	301	GAAGAAATCTCGGGCCAAAAAAGCTGACTCTAACGTATACATCAATGCGAAGCACATTGGT	360
Db	301	GAAGAAATCTCGGGCCAAAAAAGCTGACTCTAACGTATACATCAATGCGAAGCACATTGGT	360
Qy	361	GGTAACAGCGATTGGAAACTTTGAAGAAAAATGCGCAAGTTAGCTGAAATATTGAAGCCG	420
Db	361	GGTAACAGCGATTGGAAACTTTGAAGAAAAATGCGCAAGTTAGCTGAAATATTGAAGCCG	420
Qy	421	GTATTTCAATAG	432
Db	421	GTATTTCAATAG	432

RESULT 2

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US-11-251-208-52
; Sequence 52, Application US/11251208
; Publication No. US20060137043A1
; GENERAL INFORMATION:
; APPLICANT: Puzio, Piotr
; APPLICANT: Chardonens, Agnes
; APPLICANT: Shirley, Amber
; APPLICANT: Wang, Xi-Qing
; APPLICANT: Savria-Millan, Rodrigo
; APPLICANT: Mckersie, Bryan
; APPLICANT: Chen, Ruoying
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTIC
; TITLE OF INVENTION: STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED
; TITLE OF INVENTION: TOLERANCE TO ENVIRONMENTAL STRESS
; FILE REFERENCE: 13311-00015-US
; CURRENT APPLICATION NUMBER: US/11/251,208
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: PCT/US2004/011888
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: EP 03008080.8
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: EP 03009728.1
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: EP 03016672.2
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: EP 03022225.1
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(432)
US-11-251-208-52

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Db	181	TGCCCTTACTGTAAAGCTACTTTTGTCTACCTCTTCCAGAAATTGAAAGCTTCCCAATCC	240
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Db	241	AAGGCCCTTGTGTTGGAATTAGATGAAATGAGCAATGCTCAGAGATTCAAGACGCTTTA	300
Qy	301	GAAGAAATCTCGGGCCAAAAAAGCTGTACCTTAACGTTATACATCAATGGCAAGCACATTGGT	360
Db	301	GAAGAAATCTCGGGCCAAAAAAGCTGTACCTTAACGTTATACATCAATGGCAAGCACATTGGT	360
Qy	361	GGTAACAGCGATTTTGGAAACTTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTGAAGCGC	420
Db	361	GGTAACAGCGATTTTGGAAACTTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTGAAGCGC	420
Qy	421	GTATTCAATAG	432
Db	421	GTATTCAATAG	432

RESULT 3

US-11-217-529-3898

; Sequence 3898, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHIISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 3898

; LENGTH: 570

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

US-11-217-529-3898

RESULT 3

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US-11-217-529-3898
; Sequence 3898, Application US/11217529
; Publication No. US2006009612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3898
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3898

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Db 499 GGAACAGCGATTGGAAGCTTTCAAGAAAAACGGTAAATGGCTGAATATTGAAACCG 558
Qy 421 GTATTTCATA 431
Db 559 GTTTTCATA 569

RESULT 4

US-11-217-529-3588
; Sequence 3588, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3588
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3588

Query Match 35.6%; Score 153.8; DB 8; Length 345;
Best Local Similarity 67.1%; Pred. No. 1.9e-36; Indels 0; Gaps 0;
Matches 218; Conservative 0; Mismatches 107;
Qy 95 CTCACAAATGGTATCCAGGAACAGTTGCTCAGCTAAAGAGTCTGATGGCCAAAGG 154
Db 5 CTAGATATATGGTATCCAGGAACATATCGATCAGCTCAGGAACATATTGCGGAGAG 64
Qy 155 AAGTGTGTTGTCAGCAAGACATCTGCCCTTACTGTAAAGTACTTGTCTACCTCT 214
Db 65 AATTTTGGTTCGTCAGAGCTGCTGCTACTGCCAGCAGCGTTAAACACTCTGT 124
Qy 215 TCAGAAATTTGAGCTTCCCAATCCAGGCCCTTGTGTTGGAATAGATGAATGAGCA 274
Db 125 TCAGAAATTTGAGCTTCCCAATCCAGGCCCTTGTGTTGGAATAGATGAATGAGCA 184
Qy 275 ATGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCGGCCCAAAACCTGTACCTAACG 334
Db 185 ACGGCTGGATATCCAGGAGCTTTGTACAGCTCAACGCCCAAGAACCTGCGCAACA 244
Qy 335 TATACATCAATGGCAAGACATTTGGTGTAAACGCAATTTGGAACCTTTGAAGAAAATG 394
Db 245 TCTACATCAACGGTAAGCATTTGGGGGGAACGACGACTTGCAGAGAGTTGCGTGAACCG 304
Qy 395 GCAAGTTAGCTGAAATTTGAAGCC 419
Db 305 GCGAATTTGGAAGAACTCTTGGAAACC 329

RESULT 5

US-11-217-529-75707
; Sequence 75707, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75707
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75707

Query Match 33.9%; Score 146.6; DB 8; Length 333;
Best Local Similarity 65.3%; Pred. No. 2.8e-34; Indels 0; Gaps 0;
Matches 215; Conservative 0; Mismatches 114;
Qy 103 ATGGTATCCAGGAACAGTTGCTCAGTAAAGGATCTGATGGCCAAAGGAAGTGT 162
Db 1 ATGGTATCTCAAGAAACTATCAAGCAGCTCAAGGACCTTATTGCAGAAAAACGAGATCTTC 60
Qy 163 GTTCAGCAAGACATACCTGCCCTTACTGTAAAGCTACTTTGTCTACCTCTTCCAGAA 222
Db 61 GTGCGATCCAAACGTAATGCTCCATGCTGCGAGCCCTAAACACGCTTTTGAAG 120
Qy 223 TTGAAGTTTCCCAATCCAAAGCCCTTGTGTTGGAATTAGATGAAATGAGCAATGGCTCA 282
Db 121 TTAAAGTTTCCAGGTCCTCAAGTTCTGTTTTCATTTGCAATGACATGAGGAAGCGCA 180
Qy 283 GAGATTCAGACGCTTTTAGAAGAAATCTCGGCCCAAAACCTGTAACGTATACATC 342
Db 181 GACATTCAGGCTGCGTTATATGAGATTAATGCGCAAGAACCGTGCACCAATCTATATT 240
Qy 343 AATGGCAAGCAGATTCGTGTAAACGCGATTTGGAACCTTTGAAGAAAATGCAAGTTA 402
Db 241 AATGGTAAACATATTGCGGCAACGACGATTTGCGGAAATTTGAGGAGACTTGGCGAATTG 300
Qy 403 GCTGAATATTGAAGCCGCTATTTCATA 431
Db 301 GAGGAATTTGTAGAACCTATTCTTGCAAA 329

RESULT 6

US-10-953-349-37584
; Sequence 37584, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37584
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37584

Query Match 13.0%; Score 56; DB 6; Length 578;
Best Local Similarity 58.3%; Pred. No. 7.3e-07; Indels 0; Gaps 0;
Matches 98; Conservative 0; Mismatches 70;
Qy 254 TGAATTAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCGG 313
Db 182 TTGAGTTGACACTGAAAGGATGGAATGAGATTCAGTCAGCTCTTGTGTAATGGACTG 241
Qy 314 GCCAAAAAATCTGTACTTAACGTATACATCAATGGCAAGCAGCATTTGGTGAACAGCGATT 373
Db 242 GGCAGAGGACTGTTCCCAATGTCTTCATCAATGGAACACATTTGGTGGTGTGACGATA 301

QY 374 TGAACCTTTGACAAATAATGGCAAGTAGCTGAAATATTTGAAGCGG 421
DB 302 CTATTGCACTGAACAAAGGGAGGAAGCTGGTCTCTGCTGACGGAGG 349

RESULT 7

US-10-449-902-15440
; Sequence 15440, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15440
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK065962
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-15440

Query Match 12.9%; Score 55.6; DB 6; Length 575;
Best Local Similarity 60.7%; Pred. No. 9.6e-07;
Matches 91; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 254 TGAATTTAGTAATAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAAGAAATCTCGG 313
DB 172 TTGAGTTGGATGGGAGAGTGATGGATCTGAGCTGCGGACCTTGCTGAATGGACTG 231
QY 314 GCCAAAACTGTACCTACGTATACATCAATGCGCAAGCACATTTGGTGTACAGCGATT 373
DB 232 GACAAAGGACTGTTCCAAATGTCTTCATCAATGGGAAGCATATTGGTGGCTGTGATGATA 291
QY 374 TGAACCTTTGACAAATAATGGCAAGTTAG 403
DB 292 CTTGGCATTTGAACATGAAGGAAGCTGG 321

RESULT 8

US-10-449-902-4892
; Sequence 4892, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4892
; LENGTH: 729
; TYPE: DNA

; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK062117
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-4892

Query Match 12.9%; Score 55.6; DB 6; Length 729;
Best Local Similarity 60.7%; Pred. No. 1.1e-06;
Matches 91; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 254 TGAATTTAGTAATAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAAGAAATCTCGG 313
DB 326 TTGAGTTGGATGGGAGAGTGATGGATCTGAGCTGCGGACCTTGCTGAATGGACTG 385
QY 314 GCCAAAACTGTACCTACGTATACATCAATGCGCAAGCACATTTGGTGTACAGCGATT 373
DB 386 GACAAAGGACTGTTCCAAATGTCTTCATCAATGGGAAGCATATTGGTGGCTGTGATGATA 445
QY 374 TGAACCTTTGACAAATAATGGCAAGTTAG 403
DB 446 CTTGGCATTTGAACATGAAGGAAGCTGG 475

RESULT 9

US-10-449-902-279
; Sequence 279, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 279
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK058431
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-279

Query Match 12.7%; Score 55; DB 6; Length 392;
Best Local Similarity 57.1%; Pred. No. 1.2e-06;
Matches 100; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 242 AGCCCTTGTGTTGGAATTAGATGAATAAGCAATGGCTCAGAGATTCAAGACGCTTTAG 301
DB 36 AGCCCTATGTTGTGGAGCTTGATCAACGAGAGAGGATGGTTGGAGATTTCAGGATGCCCTTAT 95
QY 302 AGNAATCTCGGGCCAAAAAACTGTACCTTAACGTATACATCAATGCGCAAGCACATTTGGTG 361
DB 96 CTGACATGTTGGCAGGCGAAGCTGTTCTTCAAGTTTTTGTCCATGGGAAGCACCTGGGTG 155
QY 362 GTAACAGCGATTGTGGAACCTTTTGAAGAAAAATGGCAAGTTAGCTGAATATTGAA 416
DB 156 GCTCTGATGATACTGTTGAAGCATATGAGAGTGGCAAGCTAGCCAAACCTTTTGAA 210

RESULT 10

US-11-218-305-2985
; Sequence 2985, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:

APPLICANT: MONSANTO TECHNOLOGY, LLC
APPLICANT: McLaIRD, Paul L.
APPLICANT: Tao, Nengsheng
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
FILE REFERENCE: 38-21 (53660)B
CURRENT APPLICATION NUMBER: US/11/218,305
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US 60/606,880
PRIOR FILING DATE: 2004-09-01
NUMBER OF SEQ ID NOS: 25043
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2985
LENGTH: 885
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (10)..(10)
OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-2985

Query Match 12.7%; Score 55; DB 9; Length 885;
Best Local Similarity 57.1%; Pred. No. 1.7e-06;
Matches 100; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 242 AGCCCTTGTGGATTAGATGCAATGAGCATGGCTCAGAGATTCAAGAGCTTTAG 301
DB 363 AGCATATGTTGGAGCTTGTATGACGAGGAGTGGCTCAGAGATTCAAGAGCTTTAC 422
QY 302 AAGAAATCTCGGGCAAAAACTGTACTAACTATATACATCAATGCAAGCACATTTGGTG 361
DB 423 TTGATAGTTGGCAGCGTACTGTCTCAAGTTTGTTCATGGAAGCACCTGGTG 482
QY 362 GTAACAGCATTTGGAACTTTGAAGAAAAATGCAAGTTAGCTGAAATTTGAA 416
DB 483 GTTCTGACGATCTGTTGACTCTCTACGAAAGTGGAAACTGGCTAGACTTCTAAA 537

RESULT 11
US-11-216-545-6672
Sequence 6672, Application US/11216545
Publication No. US20060135758A1
GENERAL INFORMATION:
APPLICANT: MONSANTO Technology, LLC
APPLICANT: McLaIRD, Paul L.
APPLICANT: Tao, Nengsheng
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
FILE REFERENCE: 38-21 (53659)B
CURRENT APPLICATION NUMBER: US/11/216,545
CURRENT FILING DATE: 2005-08-31
PRIOR APPLICATION NUMBER: US 60/606,062
PRIOR FILING DATE: 2004-08-31
NUMBER OF SEQ ID NOS: 8783
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6672
LENGTH: 597
TYPE: DNA
ORGANISM: Glycine max
US-11-216-545-6672

Query Match 12.3%; Score 53.2; DB 8; Length 597;
Best Local Similarity 58.0%; Pred. No. 5.2e-06;
Matches 94; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 254 TGGATTAGTGAATGAGCAATGGCTCAGAGATTCAAGAGCTTTAGAGAAATCTCGG 313
DB 172 TTGAGTTGGACACTGAAAGCGATGGAACCTGAGATTCAAGTCTTGTGTAATGGACTG 231
QY 314 GCCAAAAAAGTGTACTTAACGTATACATCAATGCAAGCACATTTGGTGGTAAACAGCGATT 373

DB 232 GCAGAGGAGCTGTTCCTCAATGTCTTCAATGAAAAACACATCGGTGGTGTGACGATA 291
QY 374 TGGAAACTTTGAAGAAAAATGCAAGTTAGCTGAAATATTGA 415
DB 292 CTATTCAGTGAACAAGGGAGGAAGCTGTTGCTCTGCTGA 333
RESULT 12
US-10-953-349-14823
Sequence 14823, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 14823
LENGTH: 568
TYPE: DNA
ORGANISM: Glycine max
US-10-953-349-14823

Query Match 11.4%; Score 49.4; DB 6; Length 568;
Best Local Similarity 54.7%; Pred. No. 7.1e-05;
Matches 98; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 237 ATCCAAGGCCCTTGTGTGGAAATTAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGC 296
DB 186 AGCTAATTATCTCGCGCTTGAGCTCGCAAGAGAGTGTGGTAGCCAAAGTTCAATCAGC 245
QY 297 TTTAGAGAAATCTCGGGCAAAAACTGTACTTAAGTATATACATCATGCGAAGCAT 356
DB 246 TCTGGCAGAAATGACAGAGACACGCCCTGTCCCAATGTGTTCATAGGTGAAAAACACAT 305
QY 357 TGGTGTAAACAGCGATTGTGAAACTTTGAAGAAAAATGCAAGTTAGCTGAAATATTGA 415
DB 306 CGGTGGCTGGATTCTGTAAACAACTGCACAGAGAGCGCAAGTTGTTCTTATATTGA 364

RESULT 13
US-10-953-349-20411
Sequence 20411, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 20411
LENGTH: 695
TYPE: DNA
ORGANISM: Glycine max
US-10-953-349-20411

Query Match 11.4%; Score 49.2; DB 6; Length 695;
Best Local Similarity 58.0%; Pred. No. 8.9e-05;
Matches 87; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 254 TGGAAATTAGATGAAATGAGCAATGGCTCAGAGATTCAAGAGCTTTAGAGAAATCTCGG 313
DB 184 TTGAGTTGGAATGGAAGAGTGTAGCTGAGCTCCAGATGCGCTGAAGAGTGGACTG 243
QY 314 GCCAAAAAAGTGTACTTAACGTATACATCAATGCGCAAGCACATTTGGTGGTAAACAGCGATT 373

Db 244 GACAGAGGACTGTCCCAATGTCTTCATCAATGGAGCATATTTGGGGCTGTGATGATA 303

QY 374 TGGAAACTTTGAAGAAATAATGGCAAGTTAG 403

Db 304 CTATGGCACTGAACAATGATGGGAAGCTGG 333

RESULT 14

US-11-218-305-4450
; Sequence 4450, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McIlaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4450
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Zea mays
US-11-218-305-4450

Query Match 11.4%; Score 49.2; DB 9; Length 894;
Best Local Similarity 58.0%; Pred. No. 9.8e-05;
Matches 87; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 254 TCGAATAGATGAATGAGCAATGGCTCAGAGATTCAGACGCTTTAGAGAAATCTCGG 313

Db 327 TTGAGTTGGATAAGGAAAGTATGGAGCTGAGCTCCAGAAATGCCCTGAAGGAGTGGAGCTG 386

QY 314 GCCAAAAAAGTACCTAACGTATACATCAATGGCAAGCACATTTGGTGGTAACAGCGATT 373

Db 387 GACAGAGGACTGTCCCAATGTCTTCATCAATGGGAAGCATATTTGGGGCTGTGATGATA 446

QY 374 TGGAAACTTTGAAGAAATAATGGCAAGTTAG 403

Db 447 CTATGGCACTGAACAATGATGGGAAGCTGG 476

RESULT 15

US-10-449-902-17381
; Sequence 17381, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17381
; LENGTH: 790
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK067828

; DATABASE ENTRY DATE: 2001-12-06

US-10-449-902-17381

Query Match 10.9%; Score 47.2; DB 6; Length 790;

Best Local Similarity 53.9%; Pred. No. 0.00037;

Matches 97; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 222 ATTGAACGTTCCCAATCCAAGGCCCTTGTGTTGGAAATTAGATGAATGAGCAATGGCTC 281

Db 251 ATTTAGAGATCTCAAGGAGAATCCTTATATTGTTGAATCTCAGAGAGGATGGTAG 310

QY 282 AGAGATTCAAGACGCTTTTAGAAGAAATCTCGGGCCAAAAAAGTACCTAAACGTATACAT 341

Db 311 AGAAATTTCAAAGTGTCTTCTAGACTTTAGTGGCCGCTCATCTGTGCCACAGGTGTCGT 370

QY 342 CAATGGCAAGCACATTTGGTGGTAACAGCGATTGGAAACTTTGAAGAAAAAATGGCAAGTT 401

Db 371 GAATGGCCAGCACGTTGGTGGCTCAGATGATACAGCAATGCTCATTTCTAATGGACAGCT 430

Search completed: November 7, 2006, 03:39:38
Job time : 184 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 6, 2006, 19:19:05 ; Search time 41 Seconds
(without alignments)
292.088 Million cell updates/sec

Title: US-10-523-362-4
Perfect score: 714
Sequence: 1 METNFSFSDSLVILIIITL.....DLTLKNGKGLBILKPVFQ 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 320231 seqs, 83745634 residues

Total number of hits satisfying chosen parameters: 320231

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	714	100.0	143	7	US-11-251-208-53
2	223	31.2	135	6	US-10-953-349-28952
3	223	31.2	166	6	US-10-953-349-28951
4	218.5	30.6	131	6	US-10-953-349-37585
5	215.5	30.2	155	6	US-10-449-902-33357
6	215	30.1	113	6	US-10-953-349-37586
7	215	30.1	133	6	US-10-953-349-5626
8	215	30.1	135	6	US-10-953-349-5625
9	215	30.1	152	6	US-10-953-349-5624
10	209	29.3	112	6	US-10-449-902-43865
11	209	29.3	113	6	US-10-953-349-20413
12	209	29.3	131	6	US-10-953-349-20412
13	206	28.9	109	6	US-10-953-349-8856
14	206	28.9	111	6	US-10-953-349-8855
15	203	28.4	102	6	US-11-317-789A-854
16	199	27.9	109	6	US-10-953-349-14825
17	199	27.9	111	6	US-10-953-349-14824
18	185.5	26.0	131	6	US-10-449-902-45793
19	179.5	25.1	613	6	US-10-952-500-302
20	169.5	23.7	164	6	US-10-449-902-33706
21	160	22.4	579	6	US-10-952-500-294
22	159	22.3	577	6	US-10-952-500-296
23	128	17.9	100	6	US-10-953-349-4116
24	128	17.9	102	6	US-10-953-349-4115
25	127	17.8	96	6	US-10-953-349-4117

ALIGNMENTS

RESULT 1

US-11-251-208-53

; Sequence 53, Application US/11251208

; Publication No. US20060137043A1

; GENERAL INFORMATION:

; APPLICANT: Puzio, Piotr

; APPLICANT: Chardonnens, Agnes

; APPLICANT: Shirley, Amber

; APPLICANT: Wang, Xi-Qing

; APPLICANT: Sarria-Millan, Rodrigo

; APPLICANT: McKersie, Bryan

; APPLICANT: Chen, Ruoying

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTIC

; TITLE OF INVENTION: STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED

; TITLE OF INVENTION: TOLERANCE TO ENVIRONMENTAL STRESS

; FILE REFERENCE: 13311-00015-US

; CURRENT APPLICATION NUMBER: US/11/251,208

; CURRENT FILING DATE: 2005-10-14

; PRIOR APPLICATION NUMBER: PCT/US2004/011888

; PRIOR FILING DATE: 2004-04-15

; PRIOR APPLICATION NUMBER: EP 03008080.8

; PRIOR FILING DATE: 2003-04-15

; PRIOR APPLICATION NUMBER: EP 03009728.1

; PRIOR FILING DATE: 2003-05-02

; PRIOR APPLICATION NUMBER: EP 03016672.2

; PRIOR FILING DATE: 2003-08-01

; PRIOR APPLICATION NUMBER: EP 03022225.1

; PRIOR FILING DATE: 2003-09-30

; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: Patentin version 3.3

; SEQ ID NO 53

; LENGTH: 143

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

US-11-251-208-53

Query Match 100.0%; Score 714; DB 7; Length 143;

Best Local Similarity 100.0%; Pred. No. 2e-58;

Matches 143; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 METNFSFSDSLVILIIITLPTATRIIAKRFLLSTPMVSQETVAHVKDLIGQKVFVAAKTY 60

Db 1 METNFSFSDSLVILIIITLPTATRIIAKRFLLSTPMVSQETVAHVKDLIGQKVFVAAKTY 60

Qy 61 CPYCKATLSTLFOELNVPKSKALVLELDENSGSEIOTDALEESIGQKTVPNVYNGKHIG 120

Db 61 CPYCKATLSTLFOELNVPKSKALVLELDENSGSEIOTDALEESIGQKTVPNVYNGKHIG 120

Qy 121 GNSDLETLKNGKLAELKPVFQ 143
Db 121 GNSDLETLKNGKLAELKPVFQ 143

RESULT 2

US-10-953-349-28952
; Sequence 28952, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28952
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-28952

Query Match 31.2%; Score 223; DB 6; Length 135;
Best Local Similarity 38.8%; Pred. No. 2.5e-13;
Matches 47; Conservative 25; Mismatches 45; Indels 4; Gaps 3;
Qy 20 FTRIITAKRFLSTPKM--VSOETVAHVKDLIGQKEVFVAATKTPYCKATLSTLFOELNV 77
Db 9 FSVAAAAAFIALAAGSASAKTAFVKSTVKAHDVVIFSKSYCPYCKRA-KAVFKELEL 67
Qy 78 PKSKALVLELDMSGSEIQDALEELISGQKTPVNPVYINGKHIGGNSDLETLKNGKLAEL 137
Db 68 -KDPYVVELDQEDGGEIQDALSDMVGRTVPQVFIKRGHLGSGDDTVDAYENGELAKL 126

Qy 138 L 138

Db 127 L 127

RESULT 3

US-10-953-349-28951
; Sequence 28951, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28951
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-28951

Query Match 31.2%; Score 223; DB 6; Length 166;
Best Local Similarity 38.8%; Pred. No. 3.2e-13;
Matches 47; Conservative 25; Mismatches 45; Indels 4; Gaps 3;
Qy 20 FTRIITAKRFLSTPKM--VSOETVAHVKDLIGQKEVFVAATKTPYCKATLSTLFOELNV 77
Db 40 FSVAAAAAFIALAAGSASAKTAFVKSTVKAHDVVIFSKSYCPYCKRA-KAVFKELEL 98
Qy 78 PKSKALVLELDMSGSEIQDALEELISGQKTPVNPVYINGKHIGGNSDLETLKNGKLAEL 137
Db 99 -KDPYVVELDQEDGGEIQDALSDMVGRTVPQVFIKRGHLGSGDDTVDAYENGELAKL 157
Qy 138 L 138

Db 158 L 158

RESULT 4

US-10-953-349-37585
; Sequence 37585, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37585
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37585

Query Match 30.6%; Score 218.5; DB 6; Length 131;
Best Local Similarity 44.4%; Pred. No. 6.2e-13;
Matches 48; Conservative 19; Mismatches 36; Indels 5; Gaps 3;
Qy 31 STPKMVSQETVAHVKDLIGQKEVFVAATKTPYCKATLSTLFOELNVPKSKALVLELD 90
Db 12 STPEGRAM-ALAKAKEIVASAPVWFSKSYCPFC-VQVKKLFTQLG---ASFKAIELDTE 66
Qy 91 SNGSEIQDALEELISGQKTPVNPVYINGKHIGGNSDLETLKNGKLAEL 138
Db 67 SDGTETQSALAEWTGQRTVPNPVFIKRGHIGGCGDDTIALNKGKLVALL 114

RESULT 5

US-10-449-902-33357
; Sequence 33357, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205V1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33357
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-33357

Query Match 30.2%; Score 215.5; DB 6; Length 155;
Best Local Similarity 43.0%; Pred. No. 1.4e-12;
Matches 49; Conservative 19; Mismatches 41; Indels 5; Gaps 3;
Qy 25 IAKRFLSTPKMVSQETVAHVKDLIGQKEVFVAATKTPYCKATLSTLFOELNVPKSKALV 84
Db 31 IASSSSSTPES-RKWLAKAKETVASAPVVVTSKSYCPFC-VRVKKLFEQLG---ATFKA 85
Qy 85 LELDMSGSEIQDALEELISGQKTPVNPVYINGKHIGGNSDLETLKNGKLAEL 138
Db 86 IELDGSDGSELQSALEWTGQRTVPNPVFIKRGHIGGCGDDTIALNKGKLVALL 139

APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 43865
LENGTH: 112
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-43865

Query Match 29.3%; Score 209; DB 6; Length 112;
Best Local Similarity 44.9%; Pred. No. 3.9e-12;
Matches 44; Conservative 17; Mismatches 33; Indels 4; Gaps 2;

Qy 41 VAHVKDLIGQKEVFAAKTYPCKATLSTLFOELNVPKSKALVLELDMSGSEIQDAL 100
Db 3 LAKAKETVASAPVVVYSKSCPPC-VRVKLFFQLG---ATPKAIELDGESDGSSELQSA 58
Qy 101 EEISGQKTVPNVYINGKHIGGNSDLETLKKNKGKLAAIL 138
Db 59 AEWTGQRTVPNVFINGKHIGGCCDDTLALNNEGKLVPLL 96

RESULT 11
US-10-953-349-20413
Sequence 20413, Application US/109533349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 20413
LENGTH: 113
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-20413

Query Match 29.3%; Score 209; DB 6; Length 113;
Best Local Similarity 42.9%; Pred. No. 3.9e-12;
Matches 42; Conservative 23; Mismatches 29; Indels 4; Gaps 2;

Qy 41 VAHVKDLIGQKEVFAAKTYPCKATLSTLFOELNVPKSKALVLELDMSGSEIQDAL 100
Db 3 LAKAKEIVASAPLVVFSKTSPPFC-VRVKQLFEKLG---ASYKAIELDKESDGAELQNAL 58
Qy 101 EEISGQKTVPNVYINGKHIGGNSDLETLKKNKGKLAAIL 138
Db 59 KEWTGQRTVPNVFINGKHIGGCCDDTWALNNDGKLVPLL 94

RESULT 12
US-10-953-349-20412
Sequence 20412, Application US/109533349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8855
LENGTH: 111
TYPE: PRT
ORGANISM: Arabidopsis thaliana

FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 20412
LENGTH: 131
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-20412

Query Match 29.3%; Score 209; DB 6; Length 131;
Best Local Similarity 42.9%; Pred. No. 4.6e-12;
Matches 42; Conservative 23; Mismatches 29; Indels 4; Gaps 2;

Qy 41 VAHVKDLIGQKEVFAAKTYPCKATLSTLFOELNVPKSKALVLELDMSGSEIQDAL 100
Db 21 LAKAKEIVASAPLVVFSKTSPPFC-VRVKQLFEKLG---ASYKAIELDKESDGAELQNAL 76
Qy 101 EEISGQKTVPNVYINGKHIGGNSDLETLKKNKGKLAAIL 138
Db 77 KEWTGQRTVPNVFINGKHIGGCCDDTWALNNDGKLVPLL 114

RESULT 13
US-10-953-349-8856
Sequence 8856, Application US/109533349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8856
LENGTH: 109
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-8856

Query Match 28.9%; Score 206; DB 6; Length 109;
Best Local Similarity 45.7%; Pred. No. 7e-12;
Matches 43; Conservative 16; Mismatches 31; Indels 4; Gaps 2;

Qy 45 KDLIGQKEVFAAKTYPCKATLSTLFOELNVPKSKALVLELDMSGSEIQDALEEIS 104
Db 5 KEIVNSESVVFSKTYCPYC-VRVKELLOQLG---AKFKAVELDTESDSQISGLAEWT 60
Qy 105 GQKTVPNVYINGKHIGGNSDLETLKKNKGKLAAIL 138
Db 61 GQRTVPNVFINGKHIGGCCDATSNLHKDGLVPLL 94

RESULT 14
US-10-953-349-8855
Sequence 8855, Application US/109533349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8855
LENGTH: 111
TYPE: PRT
ORGANISM: Arabidopsis thaliana

US-10-953-349-8855

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Query Match      28.98; Score 206; DB 6; Length 111;
Best Local Similarity 45.78; Pred No. 7.1e-12;
Matches 43; Conservative 16; Mismatches 31; Indels 4; Gaps 2;

QY 45 KDLIGQKEVVAAKTYCPYKATLSTLTFQELNVPKSKALVLEDEMNGSEIQDALSEIS 104
      :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 7 KEVNSGVVVFKTYCPYC-VRVKELLOQLG---AKFKAVELTDSGDSIQSGLAEW 62
      :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 105 GQTVPNVYNGKHIGNSDLETLLKNGKLAEL 138
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 63 GQTVPNVFIQGNHIGGCDATSNLHKDKLVP 96
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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RESULT 15

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US-11-317-789A-854
; Sequence 854, Application US/11317789A
; Publication No. US20060168696A1
; GENERAL INFORMATION:
; APPLICANT: NADZAN, Gregory
; APPLICANT: MASCIA, Peter
; APPLICANT: FELDMANN, Kenneth A.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: CONFERRING MODULATED PLANT SIZE AND BIOMASS AND OTHER
; TITLE OF INVENTION: CHARACTERISTICS IN PLANTS
; FILE REFERENCE: 2750-1628PUS2
; CURRENT APPLICATION NUMBER: US/11/317,789A
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: 11/241,673
; PRIOR FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: 60/639,228
; PRIOR FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 965
; SEQ ID NO 854
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Ricinus communis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(102)
; OTHER INFORMATION: Public GI no. 1707981
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(102)
; FEATURE:
; LOCATION: Functional Homolog of CDNA ID no. 13489667
; LOCATION: at SEQ ID no. 839
; LOCATION: with e-value of 5.6E-12 and percent identity of 42.27
US-11-317-789A-854

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	Query Match	28.4%; Score 203; DB 7; Length 102;
	Best Local Similarity	46.8%; Pred.No.1.2e-11;
	Matches	44; Conservative 14; Mismatches 32; Indels 4; Gaps 2;
QY	45 KDLIGQKEVFVAATKTCYPYCCKTLSTLFQLNVPVPSKALVLDELDMENSGEISIDALEEIS	104
DB	7 KELVSNAVVFSKYTCPYC-TSVKKLLDQLG---AKYKVVELDTESDGSEIQTALAEWI	62
QY	105 GKQTVPNVTNGKHIGNSDLETKKNGLAEIL	138
DB	63 GORTVNPFVGGRHGGCGSHTTAKSOGOLAVPLL	96

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Job time : 42 secs

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